

STIC-Biotech/ChemLib

123629

From: Chan, Christina
Sent: Wednesday, June 02, 2004 5:44 PM
To: Holleran, Anne; STIC-Biotech/ChemLib
Subject: RE: RUSH sequence search for 09/744,197

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 & 1642
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Holleran, Anne
Sent: Wednesday, June 02, 2004 11:27 AM
To: Chan, Christina
Subject: RUSH sequence search for 09/744,197

Please approve and forward to STIC the following RUSH sequence search request. This is for an amendment due this biweek. Thanks.

Please search the following sequences for 09/744,197:

commercial and interference databases for SEQ ID NO: 1(aa)
commercial and interference database **oligomer** search of SEQ ID NO: 1(aa)

Anne Holleran
AU: 1642
Tel: (571) 272-0833
RM: Remsen, 3A14

mailbox: Remsen, 3C18

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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OK protein - protein search, using sw model

Run on: June 3, 2004, 13:26:57 ; Search time 21 Seconds
(without alignments)
673.341 Million cell updates/sec

Title: US-09-744-197-1

Perfect score: 147
Sequence: 1 MGGGWHSTQDKSLHLEGDPN.....LSITVMSDLLQINIRVAKIMK 147

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	5.4	433	2	homeotic protein H
2	8	5.4	572	2	hypothetical prote
3	8	5.4	1051	2	lmp1 protein - Myc
4	8	5.4	1365	2	lmp1 protein - Myc
5	7	4.8	111	2	hypothetical prote
6	7	4.8	161	2	GTP-binding membra
7	7	4.8	183	2	ADP-ribosylation f
8	7	4.8	185	2	ATP synthase F0 su
9	7	4.8	213	2	conserved hypotet
10	7	4.8	237	2	hypothetical prote
11	7	4.8	247	2	fbp6 protein - gar
12	7	4.8	259	2	hypothetical prote
13	7	4.8	259	2	transposase (12) B
14	7	4.8	295	2	citrate lyase beta
15	7	4.8	370	2	conserved hypotet
16	7	4.8	378	2	cystathionine gamm
17	7	4.8	402	2	hypothetical prote
18	7	4.8	415	2	mRNA-binding prote
19	7	4.8	429	2	aldehyde dehydroge
20	7	4.8	429	2	hypothetical prote
21	7	4.8	431	1	homeotic protein H
22	7	4.8	451	2	probable xanthine/
23	7	4.8	481	2	hypothetical prote
24	7	4.8	503	2	transposase (12) B
25	7	4.8	504	2	serotonin receptor
26	7	4.8	534	2	serine-rich protei
27	7	4.8	552	2	transposase (12) B
28	7	4.8	561	2	transposase (12) B
29	7	4.8	573	2	flavoprotein, 63.5

30	7	4.8	588	2	S52524	probable membrane
31	7	4.8	618	2	AD1161	two-component sens
32	7	4.8	618	2	AD1520	conserved hypotet
33	7	4.8	685	2	B69401	gene P0326 protein
34	7	4.8	747	2	S37694	heavy-metal-transp
35	7	4.8	790	1	G69071	probable membrane
36	7	4.8	804	2	AG0565	hypothetical prote
37	7	4.8	804	2	AI2157	hypothetical prote
38	7	4.8	805	2	T25795	calcium-transport
39	7	4.8	890	2	H69877	hypothetical prote
40	7	4.8	980	2	T24556	alpha-mannosidase
41	7	4.8	1036	2	AG1326	vitellogenin A2 pr
42	7	4.8	1807	2	S03124	hypothetical prote
43	7	4.8	1969	2	T38495	genome polyprotein
44	7	4.8	3005	1	GNVSTV	beta-glucosidase (
45	6	4.1	16	2	S29631	

ALIGNMENTS

RESULT 1
S20963
homeotic protein Hox B3 - mouse
N:Alternate names: homeotic protein Hox 2.7
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 20-Aug-1999
C:Accession: S20963; D42694
R:Sham, M.H.; Hunt, P.; Nonchev, S.; Papalopulu, N.; Graham, A.; Boncinelli, E.; Krumle
EMBO J. 11, 1825-1836, 1992
A:Title: Analysis of the murine Hox-2.7 gene: conserved alternative transcripts with di
A:Reference number: S20963; MUID:92258392; PMID:1582411
A:Accession: S20963
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-433 <RNA>
A:Cross-references: GB:X66177; GB:S35628; GB:S35738; NID:g3122239; PIDN:CAA46951.1; PID:
R:Nazarali, A.; Kim, Y.; Nirenberg, M.
Proc. Natl. Acad. Sci. U.S.A. 89, 2883-2887, 1992
A:Title: Hox-1.11 and Hox-4.9 homeobox genes.
A:Reference number: A42694; MUID:92212934; PMID:1348361
A:Accession: D42694
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 213-238 <NA>
A:Note: sequence extracted from NCBI backbone (NCBIN:92310, NCBI:92316)
C:Superfamily: homeotic protein Hox B3; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:192-248/Domain: homeobox homology <Hox>

Query Match
Best local similarity 100.0%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 21 PSAAPTST 28
Db 92 PSAAPTST 99

RESULT 2
B84648
hypothetical protein At2g25420 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: B84648
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Xoo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, I
euser, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:2083487; PMID:10617197
A:Accession: B84648
A:Status: preliminary

[illegible]

Db 3 SELETMETLINVFHNSGKGGDKYKSKKEIKELQTELSGFLDAQKADAVDKMKEL 62

QY 111 DEHTENKLDPEDEFMILLISTIV 132

Db 63 DENGDEVDFOEYVYVLAALTV 84

RESULT 2

BCHUIA
S-100 protein alpha chain - human
N/Alternate names: S-100 calcium-binding protein A1 (S100A1)
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1993 #sequence_revision 23-May-1997 #text_change 22-Jun-1999
C/Accession: A44470; S16740
R/Engelkamp, D.; Schaefer, B.W.; Erne, P.; Helzlsouer, C.W.
Biochemistry 31, 10258-10264, 1992
A/Title: S100 alpha, CAPL, and CACY: molecular cloning and expression analysis of three
A/Reference number: A44470; PMID:93041710; PMID:1384693
A/Accession: A44470
A/Molecule type: mRNA
A/Residues: 1-94 <ENG>
A/Cross-references: EMBL:X58079; NID:g36175; PID:CAA41107.1; PID:g36176
A/Experimental source: heart
A/Note: sequence extracted from NCBI backbone (NCBIP:116494)
C/Comment: This protein binds p53, tubulin and many other proteins at physiological conc
C/Comment: S-100 is an intracellular protein that binds calcium. It binds zinc more tightly
different affinities exist for both ions on each monomer. Physiological concentrations
binding sites.

C/Comment: Although predominant among the water-soluble brain proteins, S-100 is also found
C/Genetics: GDB:S100A1, S100A
A/Cross-references: GDB:126839; OMIM:176940
A/Map position: 1q21-1q21
C/Complex: homodimer; heterodimer with S-100 protein beta chain (see PIR:BCHUIB)
C/Superfamily: S-100 protein; calmodulin repeat homology
C/Keywords: brain; calcium binding; EF hand; heterodimer; homodimer; zinc
F/50-82/Domain: calmodulin repeat homology <EF1>
F/50-82/Domain: calmodulin repeat homology <EF2>

Query Match 17.7%; Score 131.5; DB 1; Length 94;
Best Local Similarity 32.9%; Pred. No. 0.00017;
Matches 27; Conservative 23; Mismatches 29; Indels 3; Gaps 1;

QY 54 SDLEKAIATTAIFRNSSDSG---KLEKAIKDLIQGFNPAEGQETKPKYREILSEL 110

Db 3 SELETMETLINVFHNSGKGGDKYKSKKEIKELQTELSGFLDAQKADAVDKMKEL 62

QY 111 DEHTENKLDPEDEFMILLISTIV 132

Db 63 DENGDEVDFOEYVYVLAALTV 84

RESULT 3

S35985
S-100 protein alpha chain - weatherfish
C/Species: Misgurnus fossilis (weatherfish)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: S35985
R/Ivanenko, V.V.; Gerke, V.; Minin, A.A.; Plessmann, U.; Weber, K.
Mech. Dev. 42, 151-158, 1993
A/Title: Transduction of Ca(2+) signals upon fertilization of eggs; identification of an
A/Reference number: S35985; PMID:94031845; PMID:8217841
A/Accession: S35985
A/Molecule type: protein
A/Residues: 1-95 <IVA>
C/Superfamily: S-100 protein; calmodulin repeat homology
C/Keywords: calcium binding; EF hand
F/49-81/Domain: calmodulin repeat homology <EF2>

Query Match 17.5%; Score 129.5; DB 1; Length 95;
Best Local Similarity 29.8%; Pred. No. 0.00026;
Matches 28; Conservative 27; Mismatches 34; Indels 5; Gaps 2;

QY 54 SDLEKAIATTAIFRNSSDSG---KLEKAIKDLIQGFNPAEGQETKPKYREILSEL 110

Db 2 SOLESAMESLIVFHTYSSKEGDKYKSKKEIKELQTELSGFLDAQKADAVDKMKEL 61

QY 111 DEHTENKLDPEDEFMILLISTIVMSD--LLQINRN 142

Db 62 DENGDEVDFOEYVYVLAALTVACNEFFTESMKN 95

RESULT 4

A41988
S-100 calcium-binding protein A2 - human
N/Alternate names: calcium-binding protein CAN19; S-100 calcium-binding protein L
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 29-Aug-1997
C/Accession: A41988
R/Lea, S.W.; Tomasetto, C.; Swisshelm, K.; Keyomarsi, K.; Sager, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 2504-2508, 1992
A/Title: Down-regulation of a member of the S100 gene family in mammary carcinoma cell
A/Reference number: A41988; PMID:92196147; PMID:1372446
A/Accession: A41988
A/Molecule type: mRNA
A/Residues: 1-98 <LEA>
A/Cross-references: GB:M87068; NID:g179896
A/Experimental source: mammary carcinoma cells
A/Note: sequence extracted from NCBI backbone (NCBIN:88561, NCBIP:88562)
C/Genetics: GDB:S100A2; CAN19; S100L
A/Cross-references: GDB:211118; OMIM:176993
A/Map position: 1q21-1q21
C/Superfamily: S-100 protein; calmodulin repeat homology
C/Keywords: calcium binding; EF hand
F/8-42/Domain: calmodulin repeat homology <EF1>
F/51-83/Domain: calmodulin repeat homology <EF2>

Query Match 16.6%; Score 123; DB 2; Length 98;
Best Local Similarity 31.1%; Pred. No. 0.00097;
Matches 28; Conservative 22; Mismatches 36; Indels 4; Gaps 2;

QY 53 CSDEKAIATTAIFRNSSDSG---KLEKAIKDLIQGFNPAEGQETKPKYREILSEL 109

Db 3 CSSEQALAVVATTFHFKYSCQSGDKPKLSGKKEIKELHLPFVGKXVDEBGLKLMGN 62

QY 110 DEHTENKLDPEDEFMILLISTIV--SDLLQ 138

Db 63 LDENSQGVDFQEVAVFALITVWCNDFQ 92

RESULT 5

A30129
S-100 protein, lung - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Sep-1995
C/Accession: A30129
R/Glenney Jr., J.R.; Kindy, M.S.; Zokas, L.
J. Cell Biol. 108, 569-578, 1989
A/Title: Isolation of a new member of the S100 protein family: amino acid sequence,
A/Reference number: A30129; PMID:89139574; PMID:2521861
A/Accession: A30129
A/Status: not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-97 <GLB>
C/Superfamily: S-100 protein; calmodulin repeat homology
C/Keywords: Calcium binding; EF hand
F/50-82/Domain: calmodulin repeat homology <EF2>

Query Match 15.7%; Score 116; DB 2; Length 97;
Best Local Similarity 29.2%; Pred. No. 0.0038;
Matches 26; Conservative 24; Mismatches 35; Indels 4; Gaps 2;

QY 54 SDLEKAIATTAIFRNSSDSG---KLEKAIKDLIQGFNPAEGQETKPKYREILSEL 110

Db 3 SPLQALAVVATTFHFKYSGQSGDKPKLSGKKEIKELHLPFVGKXVDEBGLKLMGN 62

N:Alternate names: neural S-100 calcium-binding protein beta
 C:Species: Homo sapiens (man)
 C>Date: 04-Dec-1986 #sequence revision 06-Jan-1995 #text_change 08-Dec-2000
 C:Accession: A38364; A32972; A03076
 R:Allore, R.J.; Friend, W.C.; O'Hallion, D.; Neilson, K.M.; Baunat, R.; Dunn, R.J.; Marks
 J. Biol. Chem. 265, 15537-15543, 1990
 A:Title: Cloning and expression of the human S100beta gene.
 A:Reference number: A38364; PMID:90368757; PMID:2394728
 A:Accession: A38364
 A:Molecule type: DNA
 A:Residues: 1-92 <RL>
 A:Cross-references: GB:J05600; GB:M59486; NID:9337726; GB:M59487; NID:9337727; GB:M59488
 R:Jensen, R.; Marshak, D.R.; Anderson, C.; Lukac, T.J.; Watterson, D.W.
 J. Neurochem. 45, 700-705, 1985
 A:Title: Characterization of human brain S100 protein fraction: amino acid sequence of S
 A:Reference number: A32972; PMID:85291729; PMID:4031854
 A:Accession: A32972
 A:Molecule type: protein
 A:Residues: 2-92 <EN>
 R:Baader, J.; Glaeser, N.; Haglid, K.; Gerard, D.
 Biochim. Biophys. Acta 790, 164-173, 1984
 A:Title: Purification, characterization and ion binding properties of human brain S100b
 A:Reference number: A30653; PMID:85023393; PMID:6487634
 A:Contents: annotation; metal ion-binding properties
 C:Comment: This protein binds p53, tubulin and many other proteins at physiological cond
 C:Comment: S-100 is an intracellular protein that binds calcium. It binds zinc more tigh
 different affinities exist for both ions on each monomer. Physiological concentrations
 nding sites.
 C:Comment: This protein is expressed predominantly in brain tissue by astroglial cells.
 C:Comment: The homodimer contains disulfide bonds, but the bond pattern has not been det
 C:Genetics:
 A:Gene: GDB:S100B
 A:Cross-references: GDB:120360; OMIM:176990
 A:Map position: 21q22.3-21q22.3
 A:Introns: 46/3
 A>Note: the first intron occurs before the initiator codon
 C:Complex: homodimer; heterodimer with S-100 protein alpha chain (see PIR:BCRUIA)
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: blocked amino end; brain; calcium binding; EF hand; heterodimer; homodimer;
 F:2-92/Product: S-100 protein beta chain status experimental <MAT>
 F:6-40/Domain: calmodulin repeat homology <EF1>
 F:49-81/Domain: calmodulin repeat homology <EF2>
 F:2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #statu
 F:19,22,24,27,32/Binding site: calcium (Ser, Glu, Asp, Lys, Glu) #status predicted
 F:62,64,66,68,73/Binding site: calcium (Asp, Asp, Asp, Glu, Glu) #status predicted

Query Match 13.3%; Score 98.5; DB 1; Length 92;
 Best Local Similarity 27.2%; Pred. No. 0.11;
 Matches 22; Conservative 21; Mismatches 35; Indels 3; Gaps 1;

QY 54 SLEKAIATLIFRNSDSDG---KLEKAIKDLQTFRNFAGQETKPKYREILSEL 110
 DB 2 SLEKAIATLIDVFQYSGREDGKRLKSKSELINNELSHLEIKQEVVDKQWETL 61

QY 111 DEHTENKLDPEDDPMILLSTIV 131
 DB 62 DNDGDGDCDFCEFMFAMVT 82

RESULT 15
 LURGIO
 calpactin I light chain - pig
 N:Alternate names: p10 protein; p11 protein
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 18-Jul-1997
 C:Accession: A03079; A24063
 R:Gerke, V.; Weber, K.
 EMBO J. 4, 2917-2920, 1985
 A:Title: The regulatory chain in the p36-kD substrate complex of viral tyrosine-specific
 A:Reference number: A03079; PMID:86055730; PMID:2996764
 A:Accession: A03079
 A:Molecule type: protein
 A:Residues: 1-95 <GER>

R:Hexham, J.M.; Totty, N.F.; Waterfield, M.D.; Crumpton, M.J.
 Biochem. Biophys. Res. Commun. 134, 248-254, 1986
 A:Title: Homology between the subunits of S100 and A 10kDa polypeptide associated wit
 A:Reference number: A24063; PMID:86130472; PMID:2936341
 A:Accession: A24063
 A:Molecule type: protein
 A:Residues: 1-51, 'XX', 54-55 <HEX>
 C:Comment: Calpactin I light does not appear to bind calcium.
 C:Comment: Calpactin I is a tetramer of two light chains and two heavy chains (annex)
 C:Function:
 A:Description: found in lamina beneath plasma membrane where it may cross-link plasm
 A:Pathway: exocytosis
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: EF hand; intestine
 F:6-37/Domain: calmodulin repeat homology <EF1>
 F:46-78/Domain: calmodulin repeat homology <EF2>

Query Match 13.0%; Score 96; DB 1; Length 95;
 Best Local Similarity 26.6%; Pred. No. 0.19;
 Matches 21; Conservative 18; Mismatches 40; Indels 0; Gaps 0;

QY 54 SLEKAIATLIFRNSDSDGKLEKAIKDLQTFRNFAGQETKPKYREILSEL 113
 DB 2 SQMHAMETWMTFFHKFAGDKGTLTREDRVLMKSPGLFNQKPLAVDKIMKDLDC 61

QY 114 TENKLDPEDDPMILLSTIV 132
 DB 62 RDGKVGQSFPSLIGLTI 80

Search completed: June 3, 2004, 13:22:27
 Job time : 21 secs

Fri Jun 4 16:16:00 2004

US-09-744-197-1.01lgo.rat

Page 1

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OM protein - protein search, using sw model

Run on: June 3, 2004, 13:29:03 ; Search time 23 Seconds
(without alignments)
329.957 Million cell updates/sec

Title: US-09-744-197-1

Perfect score: 147
Sequence: 1 MGGCMHSTQDKSLHLESDPN.....LSITVMSDLLQINIRVKIMK 147

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size: 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

- 1: /cgn2_6/prodata/2/1aa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/2/1aa/5B_COMB.pep.*
- 3: /cgn2_6/prodata/2/1aa/5A_COMB.pep.*
- 4: /cgn2_6/prodata/2/1aa/5B_COMB.pep.*
- 5: /cgn2_6/prodata/2/1aa/5A_COMB.pep.*
- 6: /cgn2_6/prodata/2/1aa/5B_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	100.0	147	US-09-621-976-7168	Sequence 7168, Ap
2	8	5.4	163	US-09-252-991A-24968	Sequence 24968, A
3	8	5.4	361	US-09-543-681A-5180	Sequence 5180, Ap
4	7	4.8	126	US-09-134-001C-3786	Sequence 3786, Ap
5	7	4.8	130	US-09-252-991A-21537	Sequence 21537, A
6	7	4.8	232	US-09-252-991A-26162	Sequence 26162, A
7	7	4.8	262	US-09-107-532A-5791	Sequence 5791, Ap
8	7	4.8	385	US-09-489-039A-13370	Sequence 13370, A
9	7	4.8	479	US-08-416-788-2	Sequence 2, Appl
10	7	4.8	816	US-08-190-802A-54	Sequence 54, Appl
11	7	4.8	816	US-08-477-346-54	Sequence 54, Appl
12	7	4.8	816	US-08-473-089-54	Sequence 54, Appl
13	7	4.8	816	US-08-487-072A-54	Sequence 54, Appl
14	7	4.8	1311	US-08-540-406-4	Sequence 4, Appl
15	7	4.8	1311	US-08-556-055-4	Sequence 4, Appl
16	7	4.8	1311	US-08-954-668-4	Sequence 4, Appl
17	7	4.8	1311	US-08-918-658-4	Sequence 4, Appl
18	7	4.8	1311	US-08-724-631-4	Sequence 4, Appl
19	7	4.8	1311	US-08-954-701A-4	Sequence 4, Appl
20	7	4.8	1311	PCT-US95-1333-4	Sequence 4, Appl
21	6	4.1	26	US-08-346-147B-45	Sequence 45, Appl
22	6	4.1	26	US-08-497-214D-45	Sequence 45, Appl
23	6	4.1	27	US-09-480-993-2	Sequence 2, Appl
24	6	4.1	27	US-09-367-065A-2	Sequence 2, Appl
25	6	4.1	27	US-09-568-466-2	Sequence 2, Appl
26	6	4.1	34	US-09-447-155B-23	Sequence 23, Appl
27	6	4.1	40	US-08-188-228-12	Sequence 12, Appl

28	6	4.1	40	1	US-08-332-643-12	Sequence 12, Appl
29	6	4.1	40	1	US-08-332-638-12	Sequence 12, Appl
30	6	4.1	40	4	US-09-480-993-18	Sequence 18, Appl
31	6	4.1	67	4	US-09-543-681A-4451	Sequence 4451, Ap
32	6	4.1	72	4	US-09-673-395A-527	Sequence 527, Ap
33	6	4.1	73	4	US-09-621-976-3908	Sequence 3908, Ap
34	6	4.1	83	2	US-08-465-380-52	Sequence 52, Appl
35	6	4.1	83	2	US-08-486-397-52	Sequence 52, Appl
36	6	4.1	83	2	US-08-486-399-52	Sequence 52, Appl
37	6	4.1	83	2	US-08-461-965-52	Sequence 52, Appl
38	6	4.1	83	2	US-08-634-641-52	Sequence 52, Appl
39	6	4.1	83	3	US-09-249-471-52	Sequence 52, Appl
40	6	4.1	83	3	US-09-249-472-52	Sequence 52, Appl
41	6	4.1	83	3	US-09-249-451-52	Sequence 52, Appl
42	6	4.1	83	3	US-08-809-455-52	Sequence 52, Appl
43	6	4.1	83	3	US-09-249-461-52	Sequence 52, Appl
44	6	4.1	83	3	US-09-249-448-52	Sequence 52, Appl
45	6	4.1	83	4	US-09-249-473-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-09-621-976-7168
; Sequence 7168, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT FILING DATE: US/09/621.976
; NUMBER OF SEQ ID NOS: 2000-07-21
; SOFTWARE: Patent.pm
; SEQ ID NO: 7168
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-7168

Query Match
Best Local Similarity 100.0%; Score 147; DB 4; Length 147;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGCMHSTQDKSLHLESDPNPSAAPTSTCAERKPKRISISKOLASVKAALCKSDLEKAI 60
DB 1 MGGCMHSTQDKSLHLESDPNPSAAPTSTCAERKPKRISISKOLASVKAALCKSDLEKAI 60
QY 61 ATTALIFNSSDSCKEKAIAKDLQTFNFAEGGTCKKREILSEDEHTEKIDF 120
DB 61 ATTALIFNSSDSCKEKAIAKDLQTFNFAEGGTCKKREILSEDEHTEKIDF 120
QY 121 EDFMILLSTVMSDLLQINIRVKIMK 147
DB 121 EDFMILLSTVMSDLLQINIRVKIMK 147

RESULT 2
US-09-252-991A-24968
; Sequence 24968, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
; FILE REFERENCE: 107196.116
; CURRENT FILING DATE: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18

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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24968
LENGTH: 163
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24968

Query Match
Best Local Similarity 5.4%; Score 8; DB 4; Length 163;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 PSAAPST 28
DB 52 PSAAPST 59

RESULT 3
US-09-543-681A-5180
Sequence 5180, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709,1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5180
LENGTH: 361
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-5180

Query Match
Best Local Similarity 5.4%; Score 8; DB 4; Length 361;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 MILLST 131
DB 167 MILLST 174

RESULT 4
US-09-134-001C-3766
Sequence 3766, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3766
LENGTH: 126
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3766

Query Match
Best Local Similarity 4.8%; Score 7; DB 4; Length 126;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 ISKOLAS 46
DB 16 ISKOLAS 22

RESULT 5
US-09-252-991A-21537
Sequence 21537, Application US/09252991A
Patent No. 6531795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21537
LENGTH: 130
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21537

Query Match
Best Local Similarity 4.8%; Score 7; DB 4; Length 130;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 PSAAPTS 27
DB 65 PSAAPTS 71

RESULT 6
US-09-252-991A-26162
Sequence 26162, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26162
LENGTH: 232
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26162

Query Match
Best Local Similarity 4.8%; Score 7; DB 4; Length 232;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 PSAAPTS 27
DB 65 PSAAPTS 71

RESULT 7
US-09-107-532A-5791
Sequence 5791, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush

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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Denke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5791:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...262
SEQUENCE DESCRIPTION: SEQ ID NO: 5791:
US-09-107-532A-5791
Query Match 4.8%; Score 7; DB 4; Length 262;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0;
QY 125 ILLSIT 131
DB 21 ILLSIT 27
RESULT 8
US-09-489-039A-13370
Sequence 13370, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13370
LENGTH: 385
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13370

Query Match 4.8%; Score 7; DB 4; Length 385;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0;
QY 43 QLASVKA 49
DB 217 QLASVKA 223
RESULT 9
US-08-416-788-2
Sequence 2, Application US/08416788
Patent No. 5780245
GENERAL INFORMATION:
APPLICANT: Marteau, Luc
TITLE OF INVENTION: No. 5780245el polypeptides Having a Serotonin
RECEPTOR ACTIVITY, Nucleic Acids Coding for These
TITLE OF INVENTION: Receptor Activity, Nucleic Acids Coding for These
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3043
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,788
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR93/01012
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92-12280
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie K.
REGISTRATION NUMBER: 38,619
REFERENCE/DOCKET NUMBER: EX92008-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3839
TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-416-788-2
Query Match 4.8%; Score 7; DB 1; Length 479;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0;
QY 46 SVKALRK 52
DB 403 SVKALRK 409
RESULT 10
US-08-190-802A-54
Sequence 54, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
US-08-190-802A-54

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: MUS MUSCULUS PROTEIN, Fig. 37
US-08-190-802A-54
Query Match 4.8%; Score 7; DB 1; Length 816;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 69 NSSSDG 75
DB 644 NSSSDG 650
RESULT 11
US-08-477-346-54
Sequence 54, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: MUS MUSCULUS PROTEIN, Fig. 37
US-08-477-346-54
Query Match 4.8%; Score 7; DB 3; Length 816;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 69 NSSSDG 75
DB 644 NSSSDG 650
RESULT 12
US-08-473-089-54
Sequence 54, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: MUS MUSCULUS PROTEIN, Fig. 37
US-08-473-089-54

Query Match 4.8%; Score 7; DB 4; Length 816;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 NSSSDSG 75
DB 644 NSSSDSG 650

RESULT 13
US-08-487-072A-54
Sequence 54, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
ATTORNEY/AGENT INFORMATION:
NAME: Ron. Dorte
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theocof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: MUS MUSCULUS PROTEIN, Fig. 37
US-08-487-072A-54
Query Match 4.8%; Score 7; DB 4; Length 816;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 69 NSSSDSG 75
DB 644 NSSSDSG 650
RESULT 14
US-08-540-406-4
Sequence 4, Application US/08540406
Patent No. 5837538
GENERAL INFORMATION:
APPLICANT: SCOTT, MATHEW P
APPLICANT: GOODRICH, LISA V

APPLICANT: JOHNSON, RONALD L
TITLE OF INVENTION: Patched Genes and their Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/540,406
FILING DATE: 06-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: a60190-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-540-406-4

Query Match 4.8%; Score 7; DB 2; Length 1311;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 LLISITV 132
DB 468 LLISITV 474

RESULT 15
US-08-656-055-4
Sequence 4, Application US/08656055
Patent No. 6027882
GENERAL INFORMATION:
APPLICANT: SCOTT, MATHEW P
APPLICANT: GOODRICH, LISA V
TITLE OF INVENTION: Patched Genes and their Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/540,406
FILING DATE:

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Page 6

ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Berttram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: a60190-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-656-055-4

Query Match 4.8%; Score 7; DB 3; Length 1311;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 LLLSTTV 132
DB 468 LLLSTTV 474

Search completed: June 3, 2004, 13:34:46
Job time: 24 secs

XX (INCY-) INCYTE PHARM INC.
XX Bandman O, Tang YT, Corley NC, Guegler KU, Baughn MR, Junning Y;
XX WPI: 2000-182695/16.
XX N-PSDB; AAZ58233.
XX New regulatory proteins and polynucleotides useful for treating and
XX detecting neurological disorders including epilepsy, Alzheimer's disease,
XX and stroke and cardiovascular disorders e.g. cardiomyopathy, myocarditis,
XX tachyarrhythmia.
XX Claim 1; Fig 1A-B; 74pp; English.
XX The present sequence is that of novel human calcium regulatory protein 1
XX (CaREG-1), as deduced from a consensus sequence (see AAZ58233) of
XX isolated cDNA clones. The protein has chemical and structural similarity
XX with human S100- α 2. Northern analysis showed that CaREG-1 is expressed
XX exclusively in lung tissue, including foetal and cancerous lung tissue.
XX The invention provides CaREG-1 and CaREG-2 polynucleotides and
XX polypeptides, expression vectors, host cells, antibodies, agonists and
XX antagonists. The polypeptides, polynucleotides and agonists are useful
XX for treating or preventing neurological disorders such as epilepsy,
XX ischaemic cerebrovascular diseases, stroke, Alzheimer's disease etc., and
XX cardiovascular disorders such as cardiomyopathy, myocarditis, Duchenne's
XX muscular dystrophy, tachyarrhythmia etc. Antagonists and vectors
XX comprising antisense sequences are useful for treating and preventing
XX cancers such as adenocarcinoma, leukaemia, lymphoma and melanoma
XX
XX Sequence 147 AA:
SQ
Query Match 100.0%; Score 147; DB 3; Length 147;
Best Local Similarity 100.0%; Pred. No. 7.8e-140; Indels 0; Gaps 0;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGCGMSTQDKSLHLEGGDPNPSAAPTSTCAPRMPKRISISQKLSVYKLRKCSDEKAI 60
Db 1 MGCGMSTQDKSLHLEGGDPNPSAAPTSTCAPRMPKRISISQKLSVYKLRKCSDEKAI 60
QY 61 ATTALIFRNSSDSGKLEKAIADLLQTOFRNFAEGQETPKYRELISLDEHTENKIDF 120
Db 61 ATTALIFRNSSDSGKLEKAIADLLQTOFRNFAEGQETPKYRELISLDEHTENKIDF 120
QY 121 EDPMILLSTVMSDLLQNIIRNVKIMK 147
Db 121 EDPMILLSTVMSDLLQNIIRNVKIMK 147
RESULT 2
ID AAM40026 standard; protein; 143 AA.
AC AAM40026;
DT 22-OCT-2001 (first entry)
DE Human polypeptide SEQ ID NO 3171.
XX Human, nocitropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemocarcin;
XX chemokine; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.
XX Homo sapiens.
XX WO200153312-A1.
XX 26-JUL-2001.
XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.
XX 21-JAN-2000; 2000US-00488725.
XX 25-APR-2000; 2000US-00552317.
XX 20-JUN-2000; 2000US-00596042.
XX 19-JUL-2000; 2000US-00620312.
XX 03-AUG-2000; 2000US-00653450.
XX 14-SEP-2000; 2000US-00662191.
XX 19-OCT-2000; 2000US-00693036.
XX 29-NOV-2000; 2000US-00727344.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang Z, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
XX Zhou P, Goodrich R, Drmanac RT;
XX WPI: 2001-442253/47.
XX N-PSDB; AAI59162.
XX Novel nucleic acids and polypeptides, useful for treating disorders such
XX as central nervous system injuries.
XX Example 4; SEQ ID NO 3171; 10078pp; English.
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
XX encoded polypeptides (AAM38642-AAM42213) with nocitropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemia and
XX C.N.S disorders. Note: The sequence data for this patent did not form
XX part of the printed specification
XX
XX Sequence 143 AA:
SQ
Query Match 97.3%; Score 143; DB 4; Length 143;
Best Local Similarity 100.0%; Pred. No. 8.2e-136; Indels 0; Gaps 0;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 MESTQDKSLHLEGGDPNPSAAPTSTCAPRMPKRISISQKLSVYKLRKCSDEKAIATTA 64
Db 1 MESTQDKSLHLEGGDPNPSAAPTSTCAPRMPKRISISQKLSVYKLRKCSDEKAIATTA 60
QY 65 LIFRNSSDSGKLEKAIADLLQTOFRNFAEGQETPKYRELISLDEHTENKIDFDFPM 124
Db 61 LIFRNSSDSGKLEKAIADLLQTOFRNFAEGQETPKYRELISLDEHTENKIDFDFPM 120
QY 125 ILLSTVMSDLLQNIIRNVKIMK 147
Db 121 ILLSTVMSDLLQNIIRNVKIMK 143
RESULT 3
ID AADU16494 standard; protein; 140 AA.
AC AADU16494;
DT 07-NOV-2001 (first entry)
DE Human novel secreted protein. Seq ID 1447.
XX Human, immunosuppressive; antiarthritic; antiinflammatory; cytostatic;
XX cardiac; vasotropic; cerebroprotective; nocitropic; neuroprotective;
XX antibacterial; virucide; fungicide; opthalmological; vulnerary;

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Page 3

KM secreted protein; rheumatoid arthritis; hyperproliferative disorder;
KM cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KM cerebral ischaemia; angiogenesis; nervous system disorder;
KM Alzheimer's disease; infection; ocular disorder; corneal infection;
KM wound healing; epithelial cell proliferation; skin ageing; food additive;
KM preservative; antiproliferative.
XX Homo sapiens.
XX OS
XX WO200155322-A2.
PD 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001341.
PF
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184668P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0218296P.
PR 14-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225477P.
PR 14-AUG-2000; 2000US-0225589P.
PR 14-AUG-2000; 2000US-0225599P.
PR 18-AUG-2000; 2000US-0226779P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226688P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229345P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230438P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232377P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.

PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234977P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 26-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235835P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 29-SEP-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239337P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241212P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249219P.
PR 17-NOV-2000; 2000US-0249224P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249255P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251865P.
PR 08-DEC-2000; 2000US-0251866P.

PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251969P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI, 2001-488783/53.
XX N-PSDB; AAS26481.
XX
XX New nucleic acid molecules encoding 461 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
XX Claim 11, SEQ ID NO 1447; 980pp; English.
XX
XX The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Antibodies to the proteins can also be used in
CC alleviating symptoms associated with the disorders and in diagnostic
CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays
CC (ELISA). Disorders which are diagnosed or treated include autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiodysplasia,
CC nervous system disorders e.g. Alzheimer's disease, infections caused by
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
CC and many other disorders listed in the specification. The polypeptides
CC can also be used to aid wound healing and epithelial cell proliferation,
CC to prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present
CC sequence represents a novel secreted protein of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC
Query Match 93.9%; Score 138; DB 4; Length 140;
Best Local Similarity 100.0%; Pred. No. 8.8e-131;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 DKSILHEDPNSAPSTGCAPRKPKRISISQSLASVLRKCSDEKAIATTAIFPN 69
Db 3 DKSILHEDPNSAPSTGCAPRKPKRISISQSLASVLRKCSDEKAIATTAIFPN 62
QY 70 SSDSDGKLEKAIANDLQTOFRNPAEGQETPKYKREILSELDEHTENKLDFFEDFILLIS 129
Db 63 SSDSDGKLEKAIANDLQTOFRNPAEGQETPKYKREILSELDEHTENKLDFFEDFILLIS 122
QY 130 ITVMSDLLONTIRNKYIMK 147
Db 123 ITVMSDLLONTIRNKYIMK 140
RESULT 4
ABUS5563
ID ABUS5563 standard; protein; 140 AA.
XX
XX ABUS5563;
XX
XX 18-MAR-2003 (first entry)
XX
XX Human novel polypeptide #650.
XX
XX Human; neural disorder; immune system disorder; renal disorder;
KW muscular disorder; respiratory disease; reproductive disorder;
KW

KW gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;
KW hyperproliferative disorder; inflammatory disease; allergic reaction;
KW blood related disorder; cancer; immunosuppressive; antiinflammatory;
KW cardiovascular; nephrotoxic; cytostatic; antiallergic; thrombolytic;
KW haemostatic; antiarteriosclerotic.
XX
XX Homo sapiens.
XX
XX US2002132753-A1.
XX
XX 19-SEP-2002.
XX
XX 17-JAN-2001; 2001US-00764864.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 22-AUG-2000; 2000US-0226688P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 08-SEP-2000; 2000US-0231413P.
PR 21-SEP-2000; 2000US-0234272P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234597P.
PR 25-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 29-SEP-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239393P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 17-NOV-2000; 2000US-0249239P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
XX
XX (ROSE/) ROSEN C A.
XX (RUBE/) RUBEN S M.
XX (BARA/) BARASH S C.
XX
XX Rosen CA, Ruben SM, Barash SC;
XX
XX WPI, 2003-147444/14.
XX N-PSDB; ABX73822.
XX
XX

XX New polypeptides and nucleic acids, useful in gene therapy for treating,
 PT inhibiting or preventing e.g. neural, immune system, muscular,
 PT respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
 PT renal disorders.
 XX
 PS Claim 11; SEQ ID NO 1447; 402pp; English.
 XX
 CC The invention relates to human novel polypeptides and their associated
 CC polynucleotides. The polypeptides and polynucleotides are useful in gene
 CC therapy for treating, inhibiting or preventing neural disorders, immune
 CC system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis
 CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g.
 CC nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders
 CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
 CC (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left
 CC heart syndrome), renal disorders (e.g. acute kidney failure and end-stage
 CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and
 CC leukaemia), inflammatory diseases (e.g. septic shock, bursts and
 CC appendicitis), allergic reactions and conditions (e.g. asthma), blood
 CC related disorders (e.g. thrombosis, atherosclerosis and myocardial
 CC infarction) and cancerous diseases. Sequences ABUS4914-ABUS5699 and
 CC ABUS5748 represent human novel polypeptides of the invention
 CC
 XX
 SQ Sequence 140 AA;
 Query Match 93.9%; Score 138; DB 6; Length 140;
 Best Local Similarity 100.0%; Pred. No. 8.8e-131;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 DKSILHEDGPNPSAAPTSTCAPRRKPKRISISKOLASVKALRKCSDELEKATATTAATTA 69
 DB 3 DKSILHEDGPNPSAAPTSTCAPRRKPKRISISKOLASVKALRKCSDELEKATATTAATTA 62
 QY 70 SSSDSGKLEKAKKLLQTOFNFAGQETPKRKEIISELDEHENTKLDPEDEPMILLLS 129
 DB 63 SSSDSGKLEKAKKLLQTOFNFAGQETPKRKEIISELDEHENTKLDPEDEPMILLLS 122
 QY 130 ITVMSDDLQNIIRNVKIMK 147
 DB 123 ITVMSDDLQNIIRNVKIMK 140
 RESULT 5
 AAM41812
 ID AAM41812 standard; protein; 137 AA.
 XX
 AC AAM41812;
 XX
 DT 22-OCT-2001 (first entry)
 DE Human polypeptide SEQ ID NO 6743.
 XX
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemoclastic;
 KW Chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW Leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO20015312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US034263.
 XX
 PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-0048725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX
 PA (HSE-) HSEQ INC.
 XX
 PI Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Dimaac RT;
 XX
 DR WPI: 2001-442253/47.
 DR N-PDBS; AA160968.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.
 XX
 PS Example 2; SEQ ID NO 6743; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and the
 CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC activation/inhibition activity, chemoclastic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening, and
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 CC
 XX
 SQ Sequence 137 AA;
 Query Match 93.2%; Score 137; DB 4; Length 137;
 Best Local Similarity 100.0%; Pred. No. 8.8e-130;
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 MESTODKSLHEDGPNPSAAPTSTCAPRRKPKRISISKOLASVKALRKCSDELEKATATTA 64
 DB 1 MESTODKSLHEDGPNPSAAPTSTCAPRRKPKRISISKOLASVKALRKCSDELEKATATTA 60
 QY 65 LIFRNSSDSGKLEKAKKLLQTOFNFAGQETPKRKEIISELDEHENTKLDPEDEPM 124
 DB 61 LIFRNSSDSGKLEKAKKLLQTOFNFAGQETPKRKEIISELDEHENTKLDPEDEPM 120
 QY 125 ILLISTVMSDDLQNIIR 141
 DB 121 ILLISTVMSDDLQNIIR 137
 RESULT 6
 AAB33229
 ID AAB33229 standard; protein; 161 AA.
 XX
 AC AAB33229;
 XX
 DT 25-JAN-2001 (first entry)
 DE Eucalyptus grandis transcription factor protein sequence #386.
 XX
 KW plant; transcription factor; gene expression; eucalyptus; pine; acacia;
 KW poplar; sweetgum; teak; manogany; bZIP; G-box binding factor;
 KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;
 KW homeodomain zipper; LIM domain; AP2; ERBBS; zinc finger domain;
 KW type 2 Cys2His2; CCAAT box element; MYB.
 XX
 OS Eucalyptus grandis.
 OS
 PN WO200053724-A2.

XX 14-SEP-2000.
 XX 09-MAR-2000; 2000WO-US006112.
 PF 11-MAR-1999; 99US-00266513.
 PR 18-AUG-1999; 99US-0149485P.
 XX
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 XX
 PI Wood M, McGrath A, Shenk MA, Glenn W;
 PI WPI; 2000-579369/54.
 DR
 XX New isolated polynucleotide encoding a plant transcription factor for
 PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
 PT having modified gene expression or modified activity of a polypeptide.
 XX
 PS Claim 8; Page 686; 747pp; English.
 XX
 CC The present invention relates to novel plant transcription factors from
 CC Eucalyptus grandis or Pinus radiata. The present sequence is one such
 CC transcription factor. The transcription factor may be used to produce a
 CC plant having modified gene expression such as a woody plant e.g. a
 CC eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or
 CC to modify the activity of a polypeptide in a plant. The transcription
 CC factors of the present invention are members from the following families
 CC of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic
 CC helix-loop-helix zipper, homeotic/homeodomain/homeobox/MAOs, homeodomain
 CC zipper, LIM domain, AP2 and EREBs, zinc finger domains of type 2
 CC Cys2His2, CCAAT box elements and MYB
 XX
 SQ Sequence 161 AA;
 XX
 Query Match 5.4%; Score 8; DB 3; Length 161;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 76 KLEKAIK 83
 DB 146 KLEKAIK 153
 RESULT 7
 AAR9637
 ID AAR9637 standard; protein; 229 AA.
 XX
 AC AAR9637;
 XX
 DT 01-OCT-1996 (first entry)
 XX
 DE Eucalyptus AGE-2 protein.
 XX
 KW Eucalyptus; reproductive gene; AGE2; Arabidopsis; agamous gene;
 KW Antirrhinum; plena gene; sterility; fertility; forest tree;
 KW transgenic plant; flower development; antisense; ribozyme.
 XX
 OS Eucalyptus globulus.
 XX
 PN AU9539013-A.
 XX
 PD 30-MAY-1996.
 XX
 PF 22-NOV-1995; 95AU-00039013.
 XX
 PR 22-NOV-1994; 94AU-00009589.
 XX
 PA (CSTR) COMMONWEALTH SCI & IND RES ORG.
 XX
 PI Harcourt RL, Llewellyn D, Kyozenka J, Peacock WJ, Southern S;
 PI Dennis ES;
 XX

DR WPI; 1996-278411/29.
 DR N-PSDB; AAT34432.
 XX
 XX Eucalyptus reproductive genes - useful for prodn. of sterile Eucalyptus
 FT trees useful for establishing wood lot plantations or in re-forestation
 FT projects.
 XX
 PS Disclosure; Page 38-39; 60pp; English.
 XX
 CC AGE-2 protein (AAR9637) is the product of a cDNA clone, AGE2 (AAT34432),
 CC isolated from Eucalyptus globulus cDNA on the basis of its homology to
 CC the Arabidopsis agamous (AG) and Antirrhinum plena (PLE) flower
 CC development genes. AGE-2 shows 62% homology to AG and 64% homology to PLE
 CC protein. AGE2 is very highly expressed in anthers and flower buds. A
 CC related protein, AGE-1 (AAR9633), was also identified. Antisense or
 CC ribozyme constructs of AGE, or of PLE2 and SOE genes (see also AAT34426
 CC and AAT34429-31), can be used to produce sterile transgenic Eucalyptus
 CC trees by minimizing inflorescence
 XX
 SQ Sequence 229 AA;
 XX
 Query Match 5.4%; Score 8; DB 2; Length 229;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 76 KLEKAIK 83
 DB 146 KLEKAIK 153
 RESULT 8
 AAE25918
 ID AAE25918 standard; protein; 314 AA.
 XX
 AC AAE25918;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Pokeweed pro-PAB-S protein.
 XX
 KW Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAB-S.
 XX
 OS Phytolacca americana.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT /note="N-terminal processed segment"
 FT Peptide 287..314
 FT /note="C-terminal processed segment"
 XX
 PN WO200233107-A2.
 XX
 PD 25-APR-2002.
 XX
 PF 15-OCT-2001; 2001WO-GB004593.
 XX
 PR 14-OCT-2000; 2000GB-00025217.
 XX
 PA (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
 XX
 PI Thomas CTR, McPherson MJ, Atkinson HU, Neelam A;
 PI WPI; 2002-489891/52.
 DR N-PSDB; AAD42715.
 XX
 XX Inducing necrotic effect in specific cells of plant by transforming plant
 PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
 PT which acts in response to application of specific stimulus to plant.
 XX
 PS Claim 24; Page 74-75; 87pp; English.
 XX
 CC The invention relates to a method of inducing a necrotic effect in
 CC specific cells of a plant. The method involves transforming the plant

CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts
CC in response to the application of a specific stimulus to the plant so as
CC to facilitate expression of a specific antiviral protein in specific
CC cells of the plant. The method is useful for inducing a necrotic effect
CC in specific cells of a plant. The present sequence is pokeweed pro-PAP-S
CC protein
CC
XX
SQ Sequence 314 AA;

Query Match 5.4%; Score 8; DB 5; Length 314;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 AAPTSTCA 30
17 AAPTSTCA 24
Db

RESULT 9
AAG32036
ID AAG32036 standard; protein; 572 AA.
XX
AC AAG32036;
XX

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 38575.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-012825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126264P.

XX 29-MAR-1999; 99US-0126785P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 08-APR-1999; 99US-0128714P.

XX 16-APR-1999; 99US-0129845P.

XX 19-APR-1999; 99US-0130077P.

XX 21-APR-1999; 99US-0130610P.

XX 23-APR-1999; 99US-0130611P.

XX 28-APR-1999; 99US-0131449P.

XX 30-APR-1999; 99US-0132048P.

XX 30-APR-1999; 99US-0132407P.

XX 04-MAY-1999; 99US-0132484P.

XX 05-MAY-1999; 99US-0132485P.

XX 06-MAY-1999; 99US-0132486P.

XX 06-MAY-1999; 99US-0132487P.

XX 07-MAY-1999; 99US-0132633P.

XX 11-MAY-1999; 99US-0134256P.

XX 14-MAY-1999; 99US-0134218P.

XX 14-MAY-1999; 99US-0134219P.

XX 14-MAY-1999; 99US-0134221P.

XX 14-MAY-1999; 99US-0134370P.

XX 18-MAY-1999; 99US-0134768P.

XX 19-MAY-1999; 99US-0134941P.

XX 20-MAY-1999; 99US-0135124P.

XX 21-MAY-1999; 99US-0135353P.

XX 24-MAY-1999; 99US-0135629P.

PR 25-MAY-1999; 99US-0136021P.

PR 27-MAY-1999; 99US-0136392P.

PR 28-MAY-1999; 99US-0136782P.

PR 01-JUN-1999; 99US-0137222P.

PR 03-JUN-1999; 99US-0137528P.

PR 04-JUN-1999; 99US-0137502P.

PR 07-JUN-1999; 99US-0137724P.

PR 08-JUN-1999; 99US-0138094P.

PR 10-JUN-1999; 99US-0138540P.

PR 14-JUN-1999; 99US-0138847P.

PR 14-JUN-1999; 99US-0139119P.

PR 16-JUN-1999; 99US-0139452P.

PR 16-JUN-1999; 99US-0139453P.

PR 17-JUN-1999; 99US-0139482P.

PR 18-JUN-1999; 99US-0139454P.

PR 18-JUN-1999; 99US-0139455P.

PR 18-JUN-1999; 99US-0139456P.

PR 18-JUN-1999; 99US-0139457P.

PR 18-JUN-1999; 99US-0139458P.

PR 18-JUN-1999; 99US-0139459P.

PR 18-JUN-1999; 99US-0139460P.

PR 18-JUN-1999; 99US-0139461P.

PR 18-JUN-1999; 99US-0139462P.

PR 18-JUN-1999; 99US-0139463P.

PR 18-JUN-1999; 99US-0139463P.

PR 18-JUN-1999; 99US-0139750P.

PR 18-JUN-1999; 99US-0139763P.

PR 21-JUN-1999; 99US-0139817P.

PR 22-JUN-1999; 99US-0139899P.

PR 23-JUN-1999; 99US-0140053P.

PR 23-JUN-1999; 99US-0140354P.

PR 24-JUN-1999; 99US-0140695P.

PR 28-JUN-1999; 99US-0140823P.

PR 29-JUN-1999; 99US-0140991P.

PR 30-JUN-1999; 99US-0141287P.

PR 01-JUL-1999; 99US-0141842P.

PR 01-JUL-1999; 99US-0142154P.

PR 02-JUL-1999; 99US-0142055P.

PR 06-JUL-1999; 99US-0142390P.

PR 08-JUL-1999; 99US-0142803P.

PR 09-JUL-1999; 99US-0142920P.

PR 12-JUL-1999; 99US-0142977P.

PR 13-JUL-1999; 99US-0143542P.

PR 14-JUL-1999; 99US-0143624P.

PR 15-JUL-1999; 99US-0144005P.

PR 16-JUL-1999; 99US-0144085P.

PR 16-JUL-1999; 99US-0144086P.

PR 19-JUL-1999; 99US-0144325P.

PR 19-JUL-1999; 99US-0144331P.

PR 19-JUL-1999; 99US-0144332P.

PR 19-JUL-1999; 99US-0144333P.

PR 19-JUL-1999; 99US-0144334P.

PR 19-JUL-1999; 99US-0144335P.

PR 20-JUL-1999; 99US-0144352P.

PR 20-JUL-1999; 99US-0144632P.

PR 20-JUL-1999; 99US-0144684P.

PR 21-JUL-1999; 99US-0144814P.

PR 21-JUL-1999; 99US-0145086P.

PR 21-JUL-1999; 99US-0145088P.

PR 22-JUL-1999; 99US-0145087P.

PR 22-JUL-1999; 99US-0145087P.

PR 22-JUL-1999; 99US-0145089P.

PR 22-JUL-1999; 99US-0145122P.

PR 22-JUL-1999; 99US-0145145P.

PR 23-JUL-1999; 99US-0145218P.

PR 23-JUL-1999; 99US-0145224P.

PR 26-JUL-1999; 99US-0145276P.

PR 27-JUL-1999; 99US-01455913P.

PR 27-JUL-1999; 99US-01455918P.

PR 28-JUL-1999; 99US-01455919P.

PR 28-JUL-1999; 99US-01455919P.

PR 02-AUG-1999; 99US-0146386P.

PR 02-AUG-1999; 99US-0146388P.

PR 02-AUG-1999; 99US-0146389P.

Query Match	Score	DB	Length	572;
Best Local Similarity	100.0%	Pred. No. 37		
Matches	8	Conservative	0	Mismatches 0; Indels 0; Gaps 0;
70	SSDSDGKL	77		
383	SSDSDGKL	390		
RESULT 10				
ID	ABB59387	standard; protein; 1577 AA.		
AC	ABB59387			
DT	26-MAR-2002	(first entry)		
XX	Drosophila melanogaster polyprotein; 1577 AA.			
XX	Drosophila; developmental biology; cell signalling; insecticide;			
XX	pharmaceutical.			
XX	Drosophila melanogaster.			
XX	WO200171042-A2.			
XX	27-SEP-2001.			
XX	23-MAR-2001; 2001WO-US009231.			
XX	23-MAR-2000; 2000US-0191637P.			
XX	11-JUL-2000; 2000US-00614150.			
XX	(PEKE) PE CORP NY.			
XX	Venter JC, Adams M, Li PMD, Myers EW;			
XX	WPI; 2001-656860/75.			
XX	N-PSDB; ABL03490.			
XX	New isolated nucleic acid detection reagent for detecting 1000 or more			
XX	genes from Drosophila and for elucidating cell signalling and cell-cell			
XX	interactions.			
XX	Disclosure; SEQ ID NO 4953; 21pp + Sequence Listing; English.			
XX	The invention relates to an isolated nucleic acid detection reagent			
XX	capable of detecting 1000 or more genes from Drosophila. The invention is			
XX	useful in developmental biology and in elucidating cell signalling and			
XX	cell-cell interactions in higher eukaryotes for the development of			
XX	insecticides, therapeutics and pharmaceutical drugs. The invention			
XX	discloses genomic DNA sequences (AB116176-AB130511), expressed DNA			
XX	sequences (AB101840-AB116175) and the encoded proteins (ABB57737-			
XX	ABB70072). The sequence data for this patent did not form part of the			
XX	printed specification, but was obtained in electronic format directly			
XX	from WIPO at ftp.wipo.int/pub/published_pct_sequences			
XX	Sequence 1577 AA;			
XX	Query Match	5.4%; Score 8; DB 4; Length 1577;		
XX	Best Local Similarity	100.0%; Pred. No. 96;		
XX	Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
XX	38	ISISKOLA 45		
XX	1409	ISISKOLA 1416		

```

ID ABB42868 standard; peptide; 41 AA.
XX
AC ABB42868;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #10374 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
EN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX
PT gene expression in human fetal liver.
XX
PS Claim 27; SEQ ID NO 35503; 639pp + Sequence Listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at http://wipo.int/pub/published\_pat\_sequences
XX
SQ Sequence 41 AA;
XX
Query Match 4.8%; Score 7; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 SAAPTST 28
DB 24 SAAPTST 30
XX
RESULT 12
ID AAM36682
XX AAM36682 standard; protein; 41 AA.
XX
AC AAM36682;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #10719 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
XX
KW genetic disorder.
XX
OS Homo sapiens.
XX
EN WO200157272-A2.

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XX 09-AUG-2001.
PD
XX
PF 30-JAN-2001; 2001WO-US000653.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human placenta.
XX
XX Claim 27; SEQ ID NO 36951; 654bp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP:
XX CC see A113115-A115756). The present sequence is a peptide encoded by one
XX CC such probe. The probes are useful for producing a microarray for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from human placenta. The probes are useful for antenatal diagnosis of
XX CC human genetic disorders
XX
XX SQ Sequence 41 AA;
XX
XX Query Match 4.8%; Score 7; DB 4; Length 41;
XX Best Local Similarity 100.0%; Pred. No. 33;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX
XX QY 22 SAAPRST 28
XX |||||
XX DB 24 SAAPRST 30
XX
XX RESULT 13
XX ABB26140
XX ID ABB26140 standard; protein; 41 AA.
XX
XX AC ABB26140;
XX
XX DT 23-JAN-2002 (first entry)
XX
XX DE Protein #8139 encoded by probe for measuring heart cell gene expression.
XX
XX KW Human; gene expression; heart; microarray; vascular system;
XX KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX KW congenital heart disease.
XX
XX OS Homo sapiens.
XX
XX PN WO200157274-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US000666.
XX
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.

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XX PI Penn SG, Hanzel DX, Chen W, Rank DR;
XX DR WPI: 2001-488899/53.
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts.
XX PS Claim 15; SEQ ID NO 27910; 530BP; English.
CC CC The present invention relates to single exon nucleic acid probes for
CC CC measuring human gene expression in a sample derived from human heart (see
CC CC AB#21535-AB#4130). The present sequence is a protein encoded by one such
CC CC probe. The probes may be used for predicting, measuring and displaying
CC CC gene expression in samples derived from the human heart via microarrays.
CC CC By measuring gene expression, the probes are useful for predicting,
CC CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC CC human heart and vascular system e.g. cardiovascular disease,
CC CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
CC CC sequence data for this patent did not form part of the printed
CC CC specification, but was obtained in electronic format directly from WIPO
CC CC at ftp.wipo.int/pub/published_pct_sequences
SQ SQ Sequence 41 AA;

Query Match 4.8%; Score 7; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 SAAPTST 28
DB 24 SAAPTST 30

RESULT 14
AAM76575
ID AAM76575 standard; protein; 41 AA.
XX AC AAM76575;
XX DT 06-NOV-2001 (first entry)
XX DD Human bone marrow expressed probe encoded protein SEQ ID NO: 36881.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; Leukaemia; Lymphoma; myeloma.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000668.
XX PS 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-0063236P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DX, Chen W, Rank DR;
XX DR WPI: 2001-488900/53.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human bone marrow.
XX PS Example 4; SEQ ID NO 36881; 658bp + Sequence Listing; English.

```

The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention

Query Match 4.8%; Score 7; DB 4; Length 41;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 SAAFTST 28
 |||||
 DB 24 SAAFTST 30

RESULT 15
 AAM63761
 ID AAM63761 standard; protein; 41 AA.
 XX AC AAM63761;
 XX DT 05-NOV-2001 (first entry)
 XX DT Human brain expressed single exon probe encoded protein SEQ ID NO: 35866.
 XX XX Human; brain expressed exon; gene expression analysis; probe; microarray;
 XX XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
 XX XX Homo sapiens.
 OS Homo sapiens.
 PN WO200157275-A2.
 PD 09-AUG-2001.
 PF 30-JAN-2001; 2001WO-US000667.
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207455P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX PT WPI; 2001-483446/52.
 XX ST Single exon nucleic acid probes for analyzing gene expression in human brains.
 XX Example 4; SEQ ID NO 35866; 650bp + Sequence listing; English.
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is a protein encoded by one of
 CC the probes of the invention
 CC
 SQ Sequence 41 AA;
 SQ Sequence 41 AA;

Query Match 4.8%; Score 7; DB 4; Length 41;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Fri Jun 4 16:15:59 2004

us-09-744-197-1.oligo.rag

Page 11

QY	22	SAAPTST	28
Db	24	SAAPTST	30

Search completed: June 3, 2004, 13:28:59
Job time : 58 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2004, 13:25:57 ; Search time 21 Seconds
(without alignments)
673.341 Million cell updates/sec

Title: US-09-744-197-1

Perfect score: 147

Sequence: 1 MGCGMSTQDKSLHGGDPN.....LSITWMDLLQNIINRYKIMK 147

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

1: PIR78:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5.4	433	2	S20963	homeotic protein H
2	5.4	572	2	B84648	hypothetical prote
3	5.4	1051	2	T18351	Imp1 protein - Myc
4	5.4	1365	2	T10822	Imp1 protein - Myc
5	4.8	111	2	AC2497	hypothetical prote
6	4.8	161	2	AS6880	GTP-binding membra
7	4.8	183	2	AS3917	ADP-ribosylation f
8	4.8	185	2	D70437	ATP synthase F0 su
9	4.8	213	2	AH2636	conserved hypotet
10	4.8	237	2	G97418	hypothetical prote
11	4.8	247	2	S60307	fibp6 protein - gar
12	4.8	259	2	T01700	hypothetical prote
13	4.8	259	2	H84148	transposase (12) B
14	4.8	255	2	H87703	citrate lyase beta
15	4.8	370	2	H69291	conserved hypotet
16	4.8	378	2	C83853	cystathionine gamm
17	4.8	402	2	E86185	hypothetical prote
18	4.8	415	2	T09213	mRNA-binding prote
19	4.8	429	2	AG3585	aldehyde dehydroge
20	4.8	429	2	S46801	hypothetical prote
21	4.8	431	1	W1026	homeotic protein H
22	4.8	451	2	AF0441	probable xanthine/
23	4.8	481	2	F71048	hypothetical prote
24	4.8	503	2	B83772	transposase (12) B
25	4.8	504	2	S27269	serotonin receptor
26	4.8	534	2	T39903	serine-rich protei
27	4.8	552	2	C83965	transposase (12) B
28	4.8	561	2	A84113	transposase (12) B
29	4.8	573	2	S75748	flavoprotein, 63.5

30	7	4.8	588	2	S52524	probable membrane
31	7	4.8	618	2	AD1161	two-component sens
32	7	4.8	618	2	AD1520	two-component sens
33	7	4.8	685	2	B69401	conserved hypotet
34	7	4.8	747	2	S37694	gene PC326 protein
35	7	4.8	790	1	G69071	heavy-metal transp
36	7	4.8	804	2	AG0565	probable membrane
37	7	4.8	805	2	A12157	hypothetical prote
38	7	4.8	805	2	T25795	hypothetical prote
39	7	4.8	890	2	H69877	calcium-transport
40	7	4.8	980	2	T24556	hypothetical prote
41	7	4.8	1036	2	AG1326	alpha-mannosidase
42	7	4.8	1807	2	S03124	vitellogenin A2 pr
43	7	4.8	1969	2	T38495	hypothetical prote
44	7	4.8	3005	1	GNVSTV	genome polypeptide
45	6	4.1	16	2	S29631	beta-glucosidase (

ALIGNMENTS

RESULT 1
S20963
homeotic protein Hox B3 - mouse
N/Alternate names: homeotic protein Hox 2.7
C/Species: Mus musculus (house mouse)
C/Date: 22-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 20-Aug-1999
C/Accession: S20963; D42694
R/Shaw, M.H.; Hunt, P.; Nonchev, S.; Papalopulu, N.; Graham, A.; Boncinelli, E.; Krum
EMBO J. 11, 1825-1836, 1992
A/Title: Analysis of the murine Hox-2.7 gene, conserved alternative transcripts with
A/Reference number: S20963; MUID:92258392; PMID:1582411
A/Accession: S20963
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-433 <SHA>
A/Cross-references: GB:X66177; GB:S35628; GB:S35738; NID:9312229; PIDN:CAA46951.1; PI
R/Nazareli, A.; Kim, Y.; Nirenberg, M.
Proc. Natl. Acad. Sci. U.S.A. 89, 2883-2887, 1992
A/Title: Hox-1.11 and Hox-4.9 homeobox genes
A/Reference number: A42694; MUID:92212934; PMID:1348361
A/Accession: D42694
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 213-238 <NAZ>
A/Note: sequence extracted from NCBI backbone (NCBIN:92310, NCBI:92316)
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Key words: DNA binding; homeobox; nucleus; transcription regulation
F:192-248/Domain: homeobox homology <HGX>

Query Match 5.4%; Score 8; DB 2; Length 433;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 PSAAPTST 28
Db 92 PSAAPTST 99

RESULT 2
B84648
hypothetical protein At2g5420 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C/Accession: B84648
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Motilac, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Unayam, L.; Tallon,
euse, D.; Nierman, W.C.; White, O.; Eisen, D.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: B84648
A/Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-572 <STC>
 A:Cross-references: GB:AE002093; NID:G4432854; PIDN:AAD20702.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: AC2925420
 A:Map position: 2

Query Match 5.4%; Score 8; DB 2; Length 572;
 Best Local Similarity 100.0%; Pred. No. 6.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 SSDBDGL 77
 |||||
 DB 383 SSDBDGL 390

RESULT 3

Imp1 protein - Mycoplasma hominis
 C:Species: Mycoplasma hominis
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999
 C:Accession: T18351
 R:Jensen, L.T.; Ladefoged, S.; Birkelund, S.; Christiansen, G.
 A:Title: Selection of Mycoplasma hominis PG21 deletion mutants by cultivation in the pre
 A:Reference number: Z18884; MUID:95369882; PMID:7543881
 A:Accession: T18351
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1051 <JEN>
 A:Cross-references: EMBL:U21961; NID:G790241; PID:G790242; PIDN:AAA81012.1
 C:Genetics:
 A:Gene: Imp1
 A:Genetic code: SGC3

Query Match 5.4%; Score 8; DB 2; Length 1051;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 A1ATTALL 66
 |||||
 DB 20 A1ATTALL 27

RESULT 4

Imp1 protein - Mycoplasma hominis
 C:Species: Mycoplasma hominis
 C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 07-Dec-1999
 C:Accession: T30822
 R:Jensen, L.T.; Ladefoged, S.; Birkelund, S.; Christiansen, G.
 A:Title: Selection of Mycoplasma hominis PG21 deletion mutants by cultivation in the pre
 A:Reference number: Z18884; MUID:95369882; PMID:7543881
 A:Accession: T30822
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1365 <JEN>
 A:Cross-references: EMBL:U21962; NID:G790243; PID:G790244; PIDN:AAA81013.1
 C:Genetics:
 A:Gene: Imp1
 A:Genetic code: SGC3

Query Match 5.4%; Score 8; DB 2; Length 1365;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 A1ATTALL 66
 |||||
 DB 20 A1ATTALL 27

RESULT 5

AC2497
 Hypothetical protein A117155 [imported] - Noctoc sp. (strain PCC 7120) plasmid pCC712
 C:Species: Noctoc sp. PCC 7120
 A:Note: Noctoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C:Accession: AC2497
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriy
 Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
 DNA Res. 6: 205-213, 2001
 A:Title: Complete genomic sequence of the filamentous nitrogen-fixing Cyanobacterium
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AC2497
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-111 <KUR>
 A:Cross-references: GB:BA000020; PIDN:BAW78239.1; PID:G17135693; GSPDB:GN00180
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: A117155
 A:Genome: plasmid

Query Match 4.8%; Score 7; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 ILSELDE 112
 |||||
 DB 103 ILSELDE 109

RESULT 6

S36680
 GMP-binding membrane protein lepA - Pseudomonas fluorescens (fragment)
 C:Species: Pseudomonas fluorescens
 C>Date: 22-Jan-1994 #sequence_revision 12-Apr-1996 #text_change 26-Aug-1999
 C:Accession: S36680; S22413
 R:Black, M.T.
 A:Title: On the catalytic mechanism of prokaryotic leader peptidase 1.
 A:Reference number: S22413; MUID:92189595; PMID:1546969
 A:Accession: S22413
 A:Molecule type: DNA
 A:Residues: 1-161 <BLA1>
 A:Cross-references: EMBL:X56466; NID:G45509; PIDN:CAA39838.1; PID:G45510
 R:Black, M.T.; Munn, U.G.R.; Allsop, A.S.
 Biochem. J. 282, 539-543, 1992
 A:Title: On the catalytic mechanism of prokaryotic leader peptidase 1.
 A:Reference number: S22413; MUID:92189595; PMID:1546969
 A:Accession: S22413
 A:Molecule type: DNA
 A:Residues: 125-161 <BLA2>
 A:Cross-references: EMBL:X56466
 C:Genetics:
 A:Gene: LepA
 C:Superfamily: GTP binding; membrane protein
 C:Keywords: GTP binding; membrane protein

Query Match 4.8%; Score 7; DB 2; Length 161;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 SVKALRK 52
 |||||
 DB 106 SVKALRK 112

RESULT 7

A53917
 ADP-ribosylation factor 3 - yeast (Saccharomyces cerevisiae)
 A:Alternate names: protein O3172; protein YOR094w; protein YOR3117w
 C:Species: Saccharomyces cerevisiae
 C>Date: 28-Oct-1994 #sequence_revision 10-Feb-1995 #text_change 02-Feb-2001
 C:Accession: A53917; S61655; S66979
 R:Lee, F.J.S.; Stevens, L.A.; Kao, Y.L.; Moss, J.; Vaughan, M.

J. Biol. Chem. 269, 20931-20937, 1994
 A>Title: Characterization of a glucocorticoid-repressible ADP-ribosylation factor 3 (ARF3) from
 A:Reference number: A53917; PMID:9434251; PMID:8063710
 A:Accession: A53917
 A:Molecule type: mRNA
 A:Residues: 1-183 <EB>
 A:Cross-references: GB:128996; NID:G576548; PIDN:AA61614.1; PID:G576549
 R:Benes, V.; Andrade, M.A.; Reckmann, S.; Teodoru, C.; Banreivi, A.; Sander, C.; Valencia
 submitted to the EMBL Data Library, December 1995
 A:Description: Nucleotide sequence and analysis of a 130 kb fragment of yeast chromosome
 A:Reference number: S61643
 A:Accession: S61655
 A:Molecule type: DNA
 A:Residues: 1-183 <BN>
 A:Cross-references: EMBL:X94335; NID:G1262139; PIDN:CAA64016.1; PID:G1164941
 R:Voss, H.; Benes, V.; Reckmann, S.; Teodoru, C.; Schwaiger, C.; Paces, V.; Ansoorge, W.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S66965
 A:Accession: S66979
 A:Molecule type: DNA
 A:Residues: 1-183 <VS>
 A:Cross-references: EMBL:Z75002; NID:G1420266; PIDN:CAA92921.1; PID:G1420267; MIPS:YOR09
 A:Experimental source: strain S288C
 A:Gene: SGD:ARF3
 C:Genetics:
 A:Map position: 15R
 C:Superfamily: ADP-ribosylation factor
 C:Keywords: blocked amino end, lipoprotein, myristylation, nucleotide binding, P-loop
 F:24-31/Region: nucleotide-binding motif A (P-loop)
 F:89-94/Region: nucleotide-binding motif B
 F:126-129/Region: GTP-binding NKXD motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:3/Modified site: aspartic acid (Asn) #status predicted

Query Match 4.8%; Score 7; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 ATTALIF 67
 |||||
 DB 84 ATTALIF 90

RESULT 8
 D70437
 ATP synthase F0 subunit b - Aquifex aeolicus
 C:Species: Aquifex aeolicus
 C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
 C:Accession: D70437
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy
 V.
 Nature 392, 353-358, 1998
 A>Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70300; PMID:9819666; PMID:9537320
 A:Accession: D70437
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-185 <MQ>
 A:Cross-references: GB:AE000746; NID:G2983925; PIDN:AA07478.1; PID:G2983925; GB:AE00065
 A:Experimental source: strain VFS
 C:Genetics:
 A:Gene: acpF2

Query Match 4.8%; Score 7; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 IAKDLLO 87
 |||||
 DB 153 IAKDLLO 159

RESULT 9
 AH2636
 conserved hypothetical protein Atu0491 [imported] - Agrobacterium tumefaciens (strain
 C:Species: Agrobacterium tumefaciens
 C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C:Accession: AH2636
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kulyavin, T.; Levy, R.; Li, M.; McCl
 i, Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
 ster, E.W.
 A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:21608550; PMID:11743193
 A:Accession: AH2636
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-213 <KUR>
 A:Cross-references: GB:AE008688; PIDN:AA41510.1; PID:G17738338; GSPDB:GN00186
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu0491
 A:Map position: circular chromosome

Query Match 4.8%; Score 7; DB 2; Length 213;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 AIAATTL 65
 |||||
 DB 98 AIAATTL 104

RESULT 10
 G97418
 hypothetical protein AGR_C 869 [imported] - Agrobacterium tumefaciens (strain C58, Ce
 C:Species: Agrobacterium tumefaciens
 C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
 C:Accession: G97418
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm
 A.; Liu, F.; Wolfram, C.; Allinger, M.; Dougherty, D.; Scott, C.; Laprae, C.; Markelz,
 Science 294, 2323-2328, 2001
 A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
 A:Reference number: A97359; PMID:21608551; PMID:11743194
 A:Accession: G97418
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-237 <KUR>
 A:Cross-references: GB:AE007869; PIDN:AAK86304.1; PID:G15155418; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR_C 869
 A:Map position: circular chromosome

Query Match 4.8%; Score 7; DB 2; Length 237;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 AIAATTL 65
 |||||
 DB 122 AIAATTL 128

RESULT 11
 S60307
 fbp6 protein - garden petunia
 C:Species: Petunia x hybrida (garden petunia)
 C>Date: 12-Apr-1996 #sequence_revision 15-Apr-1996 #text_change 24-Sep-1999
 C:Accession: S60307
 R:Angenent, G.C.; Franken, J.; Busecher, M.; Colombo, L.; van Tunen, A.J.
 Plant J. 4, 101-112, 1993
 A>Title: Petal and stamen formation in petunia is regulated by the homeotic gene fbp1
 A:Reference number: S60307; PMID:94035167; PMID:8106081
 A:Accession: S60307

A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-247 <ANG>
 C:Cross-references: EMBL:X66675; NID:g396198; PIDD:CAA48635.1; PTD:g396199
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 F:18-73/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 4.8%; Score 7; DB 2; Length 247;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 GKLEKAI 81
 DB 145 GKLEKAI 151

RESULT 12
 T01700
 hypothetical protein - maize
 C:Species: Zea mays (maize)
 C>Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 17-Nov-2000
 C:Accession: T01700; T04388
 R:Menar, M.; Ambrose, B.; Mealey, R.B.; Briggs, S.P.; Yanofsky, M.F.; Schmidt, R.J.
 unpublished results 1997, cited by EMBL
 A:Reference number: Z14402
 A:Accession: T01700
 A:Status: preliminary; translated from GB/EMBL/DDBT
 A:Molecule type: mRNA
 A:Residues: 1-259 <MEN>
 A:Cross-references: EMBL:L81162; NID:g2529339; PIDD:AA81103.1; PTD:g2529340
 A:Experimental source: strain A632
 R:Thiesen, G.; Strater, T.; Fischer, A.; Saedler, H.
 Gene 156, 155-166, 1995
 A:Title: Structural characterization, chromosomal localization and phylogenetic evaluat
 A:Reference number: Z15328; MUID:95278740; PMID:7758952
 A:Accession: T04388
 A:Status: preliminary; translated from GB/EMBL/DDBT
 A:Molecule type: mRNA
 A:Residues: 46-47; S', 49-259 <THE>
 A:Cross-references: EMBL:X81200; NID:g854645; PIDD:CAA57074.1; PTD:g1006768
 C:Genetics: ZMM2
 A:Gene: ZMM2
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 F:34-89/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 4.8%; Score 7; DB 2; Length 259;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 GKLEKAI 81
 DB 162 GKLEKAI 168

RESULT 13
 H84148
 trypsinogen (12) BH3992 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: H84148
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: H84148
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-259 <STO>
 A:Cross-references: GB:AP001520; GB:BA000004; NID:g10176401; PIDD:BA07711.1; GSPDB:GN00
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH3992

Query Match 4.8%; Score 7; DB 2; Length 259;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 LSELDH 113
 DB 10 LSELDH 16

RESULT 14
 A87703
 citrate lyase beta subunit, probable [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 24-Nov-2003
 C:Accession: A87703
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
 B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kc
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete genome sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: A87703
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-295 <STO>
 A:Cross-references: GB:AE005673; NID:g13425417; PIDD:AAK25621.1; GSPDB:GN0148
 C:Genetics:
 A:Gene: CC3655
 C:Superfamily: citrate lyase, subunit beta

Query Match 4.8%; Score 7; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 SAAPTST 28
 DB 115 SAAPTST 121

RESULT 15
 H69291
 conserved hypothetical protein AF0336 - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C:Accession: H69291
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Doc
 .; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirtness, E
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes,
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arc
 A:Reference number: A69250; MUID:98049343; PMID:9389475
 A:Accession: H69291
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-370 <KLE>
 A:Cross-references: GB:AE001081; GB:AE000782; NID:g2689404; PIDD:AA590898.1; PTD:g26;

Query Match 4.8%; Score 7; DB 2; Length 370;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 REILSEL 110
 DB 270 REILSEL 276

Search completed: June 3, 2004, 13:30:55
 Job time: 22 secs

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OM protein - protein search, using sw model

Run on: June 3, 2004, 13:14:41 ; Search time 39 Seconds
(without alignments)
1189.261 Million cell updates/sec

Title: US-09-744-197-1

Perfect score: 741
Sequence: 1 MGGCMHSTQDLSLHLEBDPN.....LSITVMSDLLQINIRKIMK 147

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541	73.0	147	11 Q8C9X1	Q8C9X1 mus musculus
2	133.5	18.0	94	11 Q9D3M4	Q9D3M4 mus musculus
3	133.5	18.0	94	11 Q91V77	Q91V77 m. 11 days e
4	122.5	16.5	101	13 Q93395	Q93395 salvelinus
5	121.5	16.4	79	11 Q9J108	Q9J108 mus musculus
6	112.5	15.2	99	13 Q8AVJ2	Q8AVJ2 squallus aca
7	108.5	14.6	100	13 Q7ZVX4	Q7ZVX4 brachydanio
8	103.5	14.0	92	11 Q925T3	Q925T3 cricetus
9	103.5	14.0	101	6 Q9TV56	Q9TV56 canis fami
10	89.5	12.1	846	10 Q7XU87	Q7XU87 oryza sativ
11	86.5	11.7	574	11 Q8C9F5	Q8C9F5 mus musculi
12	86.5	11.7	730	11 Q8BRV2	Q8BRV2 mus musculi
13	86.5	11.7	847	11 Q7TS85	Q7TS85 mus musculi
14	86	11.6	441	2 Q7X203	Q7X203 mycoplasma
15	85.5	11.5	213	4 Q9H401	Q9H401 homo sapien
16	85.5	11.5	1037	3 Q9P3K1	Q9P3K1 neurospora

17	85	11.5	351	2 Q7WWR2	Q7WWR2 mycoplasma
18	83.5	11.3	103	6 Q862H7	Q862H7 bos taurus
19	83.5	11.3	1363	5 Q81AM5	Q81AM5 plasmodium
20	83.5	11.3	2315	5 Q95ZK3	Q95ZK3 caenorhabdi
21	83.5	11.3	2396	5 Q23081	Q23081 caenorhabdi
22	83	11.2	550	11 Q80Y44	Q80Y44 mus musculi
23	83	11.2	664	11 Q7TQ66	Q7TQ66 mus musculi
24	83	11.2	1040	3 Q60177	Q60177 schizosacch
25	82.5	11.1	846	13 Q8UXK6	Q8UXK6 gallus gall
26	82.5	11.1	1390	5 Q17602	Q17602 caenorhabdi
27	82	11.1	256	4 Q9Y6Y7	Q9Y6Y7 homo sapien
28	82	11.1	326	10 Q8LEVO	Q8LEVO arabidopsis
29	82	11.1	407	10 Q9LZ43	Q9LZ43 arabidopsis
30	82	11.1	533	2 Q9R6W3	Q9R6W3 mycoplasma
31	82	11.1	888	13 Q801M7	Q801M7 xenopus lae
32	81.5	11.0	531	10 Q949U0	Q949U0 arabidopsis
33	81.5	11.0	531	10 Q9ZSA2	Q9ZSA2 arabidopsis
34	81.5	11.0	533	10 Q7XUR4	Q7XUR4 oryza sativ
35	81	10.9	432	16 Q9Z4X3	Q9Z4X3 streptomyce
36	81	10.9	664	4 Q8N5G2	Q8N5G2 homo sapien
37	81	10.9	664	4 Q9NVG6	Q9NVG6 homo sapien
38	81	10.9	2083	5 Q9N435	Q9N435 caenorhabdi
39	81	10.9	10578	5 Q81SP5	Q81SP5 caenorhabdi
40	81	10.9	18519	5 Q81SP6	Q81SP6 caenorhabdi
41	81	10.9	18534	5 Q81SP7	Q81SP7 caenorhabdi
42	80.5	10.9	523	10 Q9SE25	Q9SE25 oryza sativ
43	79.5	10.7	148	11 Q8BLX1	Q8BLX1 mus musculi
44	79.5	10.7	174	10 Q9ZVE7	Q9ZVE7 arabidopsis
45	79.5	10.7	540	10 Q81390	Q81390 nicotiana t

ALIGNMENTS

RESULT 1	Q8C9X1	PRELIMINARY;	PRT;	147 AA.
AC	Q8C9X1			
DT	01-MAR-2003 (TREMBLrel. 23, last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, last annotation update)			
DR	Hypothetical EF-hand containing protein.			
OC	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Thymus;			
RX	MEDLINE=22354683; PubMed=12466851;			
RA	The FANTOM Consortium,			
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotation of			
RT	60,770 full-length cDNAs."			
RL	Nature 420:563-573 (2002).			
DR	EMBL; AK040281; BAC30559.1;			
DR	GO; GO:000509; F:calcium ion binding; IEA.			
DR	InterPro; IPR002048; EF-hand.			
KW	Hypothetical protein.			
SQ	SEQUENCE 147 AA; 16415 MW; F1CB14DBF826D59 CRC64;			
Query Match	73.0%;	Score 541;	DB 11;	Length 147;
Best Local Similarity	72.1%;	Pred. No. 4.9e-42;		
Matches	106;	Conservative 16;	Mismatches 25;	Indels 0;
			Gaps 0;	
Qy	1 MGGCMHSTQDLSLHLEBDPN...AAPTSTCAPRKPKRISISKOLASVAKLKCSDLEKAI 60			
Db	1 MGGCMHSTQDLSLHLEBDPN...AAPTSTCAPRKPKRISISKOLASVAKLKCSDLEKAI 60			
Qy	61 ATTALIFNNSDSDGKLEKAIKADILQTFPNFAGGQRTKTKRRIILSELDHEHNTKDF 120			
Db	61 ATTALVFNNSDSDGKLEKAIKADILQTFPNFAGGQRTKTKRRIILSELDHEHNTKDF 120			

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QY 121 EDPMLILSTVMSGDLONIRYKIRK 147
DB 121 EDPVILILSTVMSGDLONIRYKIRK 147

RESULT 2
Q9DM4 PRELIMINARY: PRT: 94 AA.
Q9DM4 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE S100 calcium binding protein A1.
GN S100A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851;
RA Aizawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Konno S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schmitt L.M., Straub F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barab G.,
RA Blake J., Botelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein W.C., But C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinchik S., Hill D., Hotmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaez P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1 SIMILARITY: BELONGS TO THE S-100 FAMILY.
DR EMBL: AK017279; BAB30670.1; -.
DR HSSP: P04631; 1B4C.
DR MGD: MGI:1338917; S100a1.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR InterPro: IPR001751; CAPP_S100.
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; ethand; 1.
DR Pfam: PF01023; S_100; 1.
DR ProDom: PD003407; CAPP_S100; 1.
DR ProDom: PD000012; EF-hand; 1.
DR PROSITE: PS00018; EF_HAND; 1.
DR PROSITE: PS00303; S100 CAPP; 1.
SQ SEQUENCE 94 AA; 10487 MW; 7C8E81D135C2D15 CR664;

Query Match 18.0%; Score 133.5; DB 11; Length 94;
Best Local Similarity 34.1%; Pred. No. 8.2e-05;
Matches 28; Conservative 22; Mismatches 29; Indels 3; Gaps 1;

QY 54 SLEKATATTAIPFNSSDSG---KLEKAKDLQCPFNFAEGQETPKREITSEL 110
DB 3 SLEKAMETLIVFVFAHSGKEDKYLKSKELKDLQCPFNFAEGQETPKREITSEL 110
QY 111 DEHTKXKDFDPFILLISITY 132
DB 63 DEHTKXKDFDPFILLISITY 132
QY 111 DEHTKXKDFDPFILLISITY 132
DB 63 DEHTKXKDFDPFILLISITY 132

RESULT 3
Q91V77 PRELIMINARY: PRT: 94 AA.
Q91V77 01-JUN-2001 (TREMBlrel. 19, Created)
DT 01-JUN-2001 (TREMBlrel. 19, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE 11 days embryo cDNA, RIKEN full-length enriched library,
DE clone:270008BD09, full insert sequence (S100 calcium binding protein
DE A1) (Adult male kidney cDNA, RIKEN full-length enriched library,
DE clone:0610031F03, full insert sequence).
GN S100A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Aizawa K., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,
RA Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,
RA Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,
RA Shibata K., Shibata Y., Shingawa A., Shiraki T., Sogabe Y.,
RA Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,
RA Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:15-44(1999).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subcloning of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Komono H., Akiyama U., Nishi K., Kishimoto T., Tachino H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto K., Matsunoto H., Sakaguchi S., Ikegami T., Kasai H.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuyama S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RA Strausberg K.,
RT Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RA Du X.-J., Cole T.J., Tenis N., Gao X.-M., Kontgen F., Kemp B.E.,

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RA Heierhorst J.;
RT "Impaired cardiac contractility without cardiomyopathy in S100A1-deficient mice";
RL Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
DR EMBL; AK012578; BAB28330.1; -;
DR EMBL; BC005590; AA055590.1; -;
DR EMBL; AF368423; AA114436.1; -;
DR EMBL; AK002721; BAB22308.1; -;
DR MGI; MGI:1338917; S100a1.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR001751; CABP_S100.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 1.
DR ProDom; PD003407; CABP_S100; 1.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
SQ SEQUENCE 94 AA; 10505 MW; 7C8E817BFF36ED15 CRC64;

Query Match 18.0%; Score 133.5; DB 11; Length 94;
Best Local Similarity 34.1%; Pred. No. 8,2e-05;
Matches 26; Conservative 22; Mismatches 29; Indels 3; Gaps 1;

QY 54 SDEKAIATATLIFRNSSDSG--KLEKAIADLIQTQFRNPAAGQETKRYREISEL 110
DB 3 SELESAMETLINVFHNSGKEGDKYLSKKEKDLQTELSGFLDVQKADAVDKVMEL 62
111 DEHTENKLPEDFMILLSTIV 132
63 DENGGEVDKPEYVLAIV 84

QY 111 DEHTENKLPEDFMILLSTIV 132
DB 63 DENGGEVDKPEYVLAIV 84

Db 63 DENGGEVDKPEYVLAIV 84

RESULT 4
ID 093395 PRELIMINARY; PRT; 101 AA.
AC 093395;
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE S100-like calcium binding protein.
GN S100.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Proacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
NCBI_TaxID=8038;
RX MEDLINE=20534789; PubMed=11080585;
RA Bobe J.; Goetz F.W.;
RT "A S100 homologue mRNA isolated by differential display PCR is down-regulated in the brook trout (Salvelinus fontinalis) post-ovulatory ovary";
RL Gene 2571:187-194 (2000).
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
DR EMBL; AF077613; AAC28367.1; -;
DR HSP; P02633; 41CB.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR001751; CABP_S100.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 1.
DR ProDom; PD003407; CABP_S100; 1.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
SQ SEQUENCE 101 AA; 11285 MW; BF45582FF9279D0A CRC64;

Query Match 16.5%; Score 122.5; DB 13; Length 101;
Best Local Similarity 25.3%; Pred. No. 0.00092;

Matches 24; Conservative 28; Mismatches 40; Indels 3; Gaps 1;

QY 54 SDEKAIATATLIFRNSSDSG--KLEKAIADLIQTQFRNPAAGQETKRYREISEL 110
DB 3 SELESAMETLINVFHNSGKEGDKYLSKKEKDLQTELSGFLDVQKADAVDKVMEL 62
111 DEHTENKLPEDFMILLSTIVMSDLCNIRNVI 145
63 DONGGKVSFEERFSLVGLSTACEIYQIYHTKV 97

QY 111 DEHTENKLPEDFMILLSTIVMSDLCNIRNVI 145
DB 63 DONGGKVSFEERFSLVGLSTACEIYQIYHTKV 97

Db 63 DONGGKVSFEERFSLVGLSTACEIYQIYHTKV 97

RESULT 5
ID 09108 PRELIMINARY; PRT; 79 AA.
AC 09108;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE S100 calcium binding protein A1 (Fragment).
GN S100A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RX [1]
RT "Transcriptional regulation of S100A1 and expression during mouse heart development";
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
DR EMBL; AF218353; AAF32320.1; -;
DR HSP; P04631; 1B4C.
DR MGI; MGI:1338917; S100a1.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR001751; CABP_S100.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 1.
DR ProDom; PD003407; CABP_S100; 1.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
FT NON TER 79
SQ SEQUENCE 79 AA; 8863 MW; F94EDA3A798615D5 CRC64;

Query Match 16.4%; Score 121.5; DB 11; Length 79;
Best Local Similarity 33.8%; Pred. No. 0.00084;
Matches 26; Conservative 20; Mismatches 28; Indels 3; Gaps 1;

QY 54 SDEKAIATATLIFRNSSDSG--KLEKAIADLIQTQFRNPAAGQETKRYREISEL 110
DB 3 SELESAMETLINVFHNSGKEGDKYLSKKEKDLQTELSGFLDVQKADAVDKVMEL 62
111 DEHTENKLPEDFMILL 127
63 DENGGEVDKPEYVLAIV 79

QY 111 DEHTENKLPEDFMILL 127
DB 63 DENGGEVDKPEYVLAIV 79

Db 63 DENGGEVDKPEYVLAIV 79

RESULT 6
ID 08AVJ2 PRELIMINARY; PRT; 99 AA.
AC 08AVJ2;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE S-100 calcium-binding protein A1.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Squalidae; Squalus.
NCBI_TaxID=7797;
RX [1]
RT SEQUENCE FROM N.A.

RA Wang C., Callard G.V.;
 RT "Molecular cloning and stage dependence of an S-10 CDNA from the shark
 RT testis.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF421551; AAN63527.1; -
 DR GO: GO:0005509; F:calcium ion binding; IEA.
 DR InterPro: IPR001751; CABP_S100.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 1.
 DR Pfam: PF01023; S_100; 1.
 DR ProDom: PD003407; CABP_S100; 1.
 DR ProDom: PD000012; EF-hand; 1.
 DR SMART: SMO0054; Efn; 1.
 DR PROSITE: PS00018; EF_HAND; 1.
 DR PROSITE: PS00303; S100_CABP; 1.
 SQ SEQUENCE 99 AA; 11050 MW; BA62D8190A4A3693 CRC64;

Query Match 15.2%; Score 112.5; DB 13; Length 99;
 Best Local Similarity 30.0%; Pred. No. 0.0074;
 Matches 24; Conservative 22; Mismatches 31; Indels 3; Gaps 1;

CY 54 SDLEKATATLIRFNSSDSG--KLEKAIADLQTOFRNPAEGQETPKYREILSEL 110
 DB 2 TELESMAAGITGVRRKSGKSGKXSSNNEMVDLKAELPRLKSGOKAAVDKIMKL 61
 CY 111 DEHTENKLDPEDFMILLIST 130
 DB 62 DRNDGELDFQEFVLLAL 81

RESULT 7

ID Q7ZVA4 PRELIMINARY; PRT; 100 AA.
 AC Q7ZVA4;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Eubryotia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 CC Cyprinidae; Danio.
 CC NCBI_Taxid=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Body;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC045941; AAN45941.1; -
 DR GO: GO:0005509; F:calcium ion binding; IEA.
 DR InterPro: IPR001751; CABP_S100.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 1.
 DR Pfam: PF01023; S_100; 1.
 DR ProDom: PD003407; CABP_S100; 1.
 DR SMART: SMO0054; Efn; 1.
 DR PROSITE: PS00018; EF_HAND; 1.
 DR PROSITE: PS00303; S100_CABP; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 100 AA; 11157 MW; DAB8181AE54CB8C8 CRC64;

Query Match 14.6%; Score 108.5; DB 13; Length 100;
 Best Local Similarity 25.3%; Pred. No. 0.018;
 Matches 22; Conservative 28; Mismatches 34; Indels 3; Gaps 1;

CY 54 SDLEKATATLIRFNSSDSG--LEKAIADLQTOFRNPAEGQETPKYREILSEL 110
 DB 3 SDLEKATATLIRFNSSDSG--LEKAIADLQTOFRNPAEGQETPKYREILSEL 62
 CY 111 DEHTENKLDPEDFMILLIST 137
 DB 63 DANGDEVNFEFEVLVGLSIACPOL 89

RESULT 8

ID Q925T3 PRELIMINARY; PRT; 92 AA.
 AC Q925T3;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE S100B.
 OS Cricetus griseus (Chinese hamster).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Cricetus.
 CC NCBI_Taxid=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kuse O., Yamakawa Y., Nishijima M.;
 RT "Enhancement of transport-dependent decarboxylation of
 RT phosphatidylserine by S100B protein in permeabilized Chinese hamster
 RT ovary cells.";
 RL J. Biol. Chem. 0:0-0(2001).
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 DR EMBL: AB056121; BAB43945.1; -
 DR GO: GO:0005737; C:cytoplasm; ISS.
 DR GO: GO:0005576; C:extracellular; ISS.
 DR GO: GO:0005509; F:calcium ion binding; ISS.
 DR GO: GO:0019210; F:kinase inhibitor activity; ISS.
 DR GO: GO:0042803; F:protein homodimerization activity; ISS.
 DR GO: GO:0048155; F:S100 alpha binding; ISS.
 DR GO: GO:0048154; F:S100 beta binding; ISS.
 DR GO: GO:0048156; F:tau protein binding; ISS.
 DR GO: GO:0008270; F:zinc ion binding; ISS.
 DR GO: GO:0048143; F:astrocyte activation; ISS.
 DR GO: GO:0007409; P:axonogenesis; ISS.
 DR GO: GO:0006874; P:calcium ion homeostasis; ISS.
 DR GO: GO:0006112; P:energy reserve metabolism; ISS.
 DR GO: GO:0048151; P:hyperphosphorylation; ISS.
 DR GO: GO:0006917; P:induction of apoptosis; ISS.
 DR GO: GO:0007611; P:learning and/or memory; ISS.
 DR GO: GO:0045917; P:positive regulation of complement activation; ISS.
 DR GO: GO:0042035; P:regulation of long-term neuronal synaptic P...; ISS.
 DR GO: GO:0048169; P:regulation of protein biosynthesis; ISS.
 DR GO: GO:0006417; P:regulation of protein biosynthesis; ISS.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001751; CABP_S100.
 DR Pfam: PF00036; ehand; 1.
 DR ProDom: PD003407; CABP_S100; 1.
 DR PROSITE: PS00018; EF_HAND; 1.
 DR PROSITE: PS00303; S100_CABP; 1.
 SQ SEQUENCE 92 AA; 10749 MW; AP50107EC2BEDFEB CRC64;

Query Match 14.0%; Score 103.5; DB 11; Length 92;
 Best Local Similarity 29.6%; Pred. No. 0.046;
 Matches 24; Conservative 20; Mismatches 34; Indels 3; Gaps 1;

CY 54 SDLEKATATLIRFNSSDSG--KLEKAIADLQTOFRNPAEGQETPKYREILSEL 110
 DB 2 SELEKAVVALIDIFHQYSGREGXKDKSKSELKELINNELSHFLEIRKQGVVDKVMET 61
 CY 111 DEHTENKLDPEDFMILLIST 131
 DB 62 DEDDGDGCDPQEFMAFVSWT 82

RESULT 9

ID Q9TV56 PRELIMINARY; PRT; 101 AA.
 AC Q9TV56;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Metastasin.

QY 53 CSDEKAIATATLIFNNSSDSGKLE-----KAIKDLLOTOFNFAGQETKPKY 103
 DB 282 CSGESAIISNDYISKTEKEDVKLKECSKRANNGFTLRDLVPMQKRVL-----KY 334
 QY 104 REITSELDENTENKLPEDFMILLISITVMSDLLONIRVK 144
 DB 335 HLLQELVKATHDPEMERKAN---LKLALDAMKDLAQVNEVK 372
 RESULT 12
 ID Q7S85 PRELIMINARY; PRT; 730 AA.
 AC Q7S85
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Vav 3 oncogene (Fragment).
 GN VAV3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RX NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta, and Vein;
 RX MEDLINE=22354683; PubMed=12466851;
 RA THE PANTOM Consortium,
 RA The Riken Genome Exploration Research Group Phase I & II Team,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR EMBL; AK041249; BAC30879.1; -
 DR PIR; P70558; P70677.
 DR MGD; MGI:1886519; Vav3.
 DR GO; GO:0005085; P:guanylyl-nucleotide exchange factor activity; IEA.
 DR GO; GO:0016491; P:oxidoreductase activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002086; Aldohyde dehydr.
 DR InterPro; IPR003447; CH type.
 DR InterPro; IPR002219; DAG PE-bind.
 DR InterPro; IPR001331; GDS_CDC24.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR000219; RHOGEF.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00307; CH; 1.
 DR Pfam; PF00130; DAG PE-bind; 1.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00621; RHOGEF; 1.
 DR Pfam; PF00017; SH2; 1.
 DR PRINTS; PR00688; SM22CALPONIN.
 DR ProDom; PD001527; CH type; 1.
 DR ProDom; PD00093; SH2; 1.
 DR SMART; SM00109; C1; 1.
 DR SMART; SM00033; CH; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00325; RHOGEF; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; 1.
 DR PROSITE; PS00021; CH; 1.
 DR PROSITE; PS00479; DAG PE BIND_DOM_1; 1.
 DR PROSITE; PS00061; DAG PE BIND_DOM_2; 1.
 DR PROSITE; PS00741; DH_1; 1.
 DR PROSITE; PS0010; DH_2; 1.
 DR PROSITE; PS00003; PH_DOMAIN; 1.
 DR PROSITE; PS00001; SH2; 1.
 DR PROSITE; PS00002; SH3; 1.
 DR NON_TER 730
 FT SEQUENCE 730 AA; 84432 MW; 63A9E137D32C47B CRC64;

Query Match 11.7%; Score 86.5; DB 11; Length 847;
 Best Local Similarity 28.7%; Pred. No. 23;
 Matches 29; Conservative 14; Mismatches 39; Indels 19; Gaps 3;
 QY 53 CSDEKAIATATLIFNNSSDSGKLE-----KAIKDLLOTOFNFAGQETKPKY 103
 DB 282 CSGESAIISNDYISKTEKEDVKLKECSKRANNGFTLRDLVPMQKRVL-----KY 334
 QY 104 REITSELDENTENKLPEDFMILLISITVMSDLLONIRVK 144
 DB 335 HLLQELVKATHDPEMERKAN---LKLALDAMKDLAQVNEVK 372
 RESULT 13
 ID Q7S85 PRELIMINARY; PRT; 847 AA.
 AC Q7S85
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Vav 3 oncogene.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RX NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=22368257; PubMed=12477932;
 RA Strauberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
 RA Klausner R.D.; Collins F.S.; Wagner L.; Shemen C.M.; Schuler G.D.;
 RA Altschul S.F.; Zeeberg B.; Buecaw K.H.; Schaefer C.F.; Bhat N.K.;
 RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
 RA Ditschenko L.; Marzina K.; Parter A.A.; Rubin G.M.; Hong L.;
 RA Stapleton M.; Soares M.B.; Bonardo M.; Cavaletto T.L.; Schetz T.F.;
 RA Brownstein W.J.; Udell T.B.; Tohyuki S.; Carninci P.; Prange C.J.;
 RA Rana S.S.; Loguettano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.;
 RA Bobak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
 RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
 RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
 RA Faley J.; Helton E.; Kettman M.; Madan A.; Rodriguez S.; Sanchez A.;
 RA Whitting M.; Madan A.; Young A.C.; Shevchenko V.; Bouffard G.G.;
 RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
 RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;
 RA Kravitski M.I.; Skalska U.; Smalins D.E.; Scherch A.; Schein J.E.;
 RA Jones S.J.; Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA Strauberg R.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC052739; AAH52739.1; -
 SQ SEQUENCE 847 AA; 97967 MW; 727C9BF50DF8CF19 CRC64;
 Query Match 11.7%; Score 86.5; DB 11; Length 847;
 Best Local Similarity 28.7%; Pred. No. 23;
 Matches 29; Conservative 14; Mismatches 39; Indels 19; Gaps 3;
 QY 53 CSDEKAIATATLIFNNSSDSGKLE-----KAIKDLLOTOFNFAGQETKPKY 103
 DB 282 CSGESAIISNDYISKTEKEDVKLKECSKRANNGFTLRDLVPMQKRVL-----KY 334
 QY 104 REITSELDENTENKLPEDFMILLISITVMSDLLONIRVK 144
 DB 335 HLLQELVKATHDPEMERKAN---LKLALDAMKDLAQVNEVK 372
 RESULT 14
 ID Q7X203 PRELIMINARY; PRT; 441 AA.

AC 07X203; (TRENBLREL. 25, Created)
 DT 01-OCT-2003 (TRENBLREL. 25, last sequence update)
 DT 01-OCT-2003 (TRENBLREL. 25, last annotation update)
 DE AVGC.
 GN MYCOPLASMA AGALACTIAE.
 OS Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OC NCBI_TaxID=2110;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=variant 627#3;
 RX MEDLINE=22703458; PubMed=12819065;
 RA Filtman-Tene R., Mudani-Orenstein S., Levisohn S., Yegor D.;
 RT "Variable Lipoprotein Genes of Mycoplasma agalactiae Are Activated in
 Vivo by Promoter Addition via Site-Specific DNA Inversions.";
 RL Infect. Immun. 71:3821-3830(2003).
 DR EMBL:AY195887; AAC39838.1;
 SQ SEQUENCE 441 AA; 46964 MW; 6D3B960594880B8 CRC64;

Query Match 11.6%; Score 86; DB 2; Length 441;
 Best Local Similarity 24.0%; Pred. No. 12;
 Matches 37; Conservative 27; Mismatches 58; Indels 32; Gaps 6;

QY 19 PNEAAPTSTCAPKMKRISISKOLA-----SVK-----ALRCSDEKAIATTL- 65
 DB 57 PNPGLTPTSTPAKPGKTPERNADTVDSGADISGSKTPDTTATKSLDKLTIANNNLG 116
 QY 66 ---IFRNSSDSGKLEKAIADLQTFRNFAEGQETPKYREILSELDEHT--ENKLD 120
 DB 117 KVGYSKKEKKEKEVEEIKTALV-----AKVTLKKGKDLKADLSKNSVVSND 169
 QY 121 EDFMILLISTV-----MSDLLQNTIRNVKIMK 147
 DB 170 EGEVTLKEFEVETSSGAKAKLSDALKTIANNNGK 203

RESULT 15

Q9H4U1 PRELIMINARY; PRT; 213 AA.
 AC Q9H4U1;
 DT 01-MAR-2001 (TRENBLREL. 16, Created)
 DT 01-MAR-2001 (TRENBLREL. 16, last sequence update)
 DT 01-OCT-2003 (TRENBLREL. 25, last annotation update)
 DE DJ14N1.2 (Novel S-100/ICBP type calcium binding protein,
 similar to trichohyalin) (Fragment).
 GN DJ14N1.2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Laird G.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: BELONGS TO THE S-100 FAMILY.
 DR EMBL: AL356504; CAC13173.1; -.
 DR HSSP: P02638; ICFP.
 GO: GO:0005509; F:calcium ion binding; IEA.
 DR InterPro: IPR001751; CACP_S100.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF01023; S_100; 1.
 DR PROSITE: PS00018; EF_HAND; 1.
 DR PROSITE: PS00303; S100_CABP; 1.
 FT NON_TER 213
 SQ SEQUENCE 213 AA; 24340 MW; B8C6E0810098E7D2 CRC64;

Query Match 11.5%; Score 85.5; DB 4; Length 213;
 Best Local Similarity 23.2%; Pred. No. 5.6;
 Matches 19; Conservative 22; Mismatches 38; Indels 3; Gaps 1;

DB 2 TDLRSVTVTVIDVYKTKTKDGECCGTSKSEKELKEKELHPVAKNDDDDPTVDVIVEMTL 61
 QY 111 DEHTENKLDPEDEFMILLISTV 132
 DB 62 DRDHRRLDFTTEFLIMFKLTM 83
 Search completed: June 3, 2004, 13:21:23
 Job time : 39 secs

54 SDEKAIATTLATFRNSSDSGK--LEKAIADLQTFRNFAEGQETPKYREILSEL 110

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: June 3, 2004, 13:17:56 ; Search time 18 Seconds

(without alignments)
425,240 Million cell updates/sec

Title: US-09-744-197-1

Sequence: 1 MGGCMSTQDKSLHLEBDN.....LSITVMDLLGNINVKMK 147

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt 42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138.5	18.7	93	1 S10A_RAT	P35467 ratu
2	133.5	18.0	93	1 S10A_MOUSE	P56565 mus muscu
3	132.5	17.9	93	1 S10A_BOVIN	P20239 bos tauru
4	131.5	17.7	93	1 S10A_HUMAN	P23297 homo sapien
5	123	16.6	97	1 S10A_HUMAN	P29034 homo sapien
6	116	15.7	97	1 S10A_BOVIN	P10462 bos tauru
7	106.5	14.4	101	1 S10A_HUMAN	P26447 homo sapien
8	103.5	14.0	91	1 S10B_MOUSE	P50114 mus muscu
9	102.5	13.8	91	1 S10B_RAT	P04631 ratu
10	102.5	13.8	100	1 S10A_MOUSE	P35466 bos tauru
11	102.5	13.8	101	1 S10A_BOVIN	P07091 mus muscu
12	102.5	13.8	122	1 S10A_BOVIN	P26783 bos tauru
13	101.5	13.7	91	1 S10B_BOVIN	P02638 bos tauru
14	99.5	13.4	101	1 S10A_RAT	P05842 ratu
15	98.5	13.3	91	1 S10B_HUMAN	P04271 homo sapien
16	97.5	13.2	98	1 S10A_HUMAN	P04271 homo sapien
17	96	13.0	95	1 S10A_PIG	P04263 sus scrofa
18	96	13.0	96	1 S10A_HUMAN	P08206 homo sapien
19	96	13.0	101	1 S10A_BOVIN	P08206 homo sapien
20	96	13.0	112	1 S10A_BOVIN	P08206 homo sapien
21	95.5	12.9	119	1 M126_CHICK	P28318 gallu
22	95	12.8	96	1 S10A_MOUSE	P08207 mus muscu
23	94.5	12.8	88	1 S10A_RAT	P50115 ratu
24	91.5	12.3	88	1 S10A_MOUSE	P27003 mus muscu
25	91	12.3	96	1 S10A_CHICK	P27003 gallu
26	89.5	12.1	95	1 S10A_HUMAN	P25815 homo sapien
27	89	12.0	94	1 S10A_RAT	P06702 ratu
28	89	12.0	114	1 S10A_HUMAN	P24479 gallu
29	86.5	11.7	101	1 S10A_CHICK	P08206 mus muscu
30	86.5	11.7	847	1 VAV3_MOUSE	P02633 bos tauru
31	86	11.6	78	1 S10A_BOVIN	P08206 mus muscu
32	85	11.5	8545	1 ANCA_CAEEL	P08206 mus muscu
33	84	11.3	78	1 S10A_PIG	P02632 sus scrofa

34	83.5	11.3	843	1 VAV3_RAT	P54100 ratu
35	83.5	11.3	847	1 VAV3_HUMAN	P08206 mus muscu
36	81.5	11.0	98	1 S11_MOUSE	P50543 mus muscu
37	81.5	11.0	779	1 IP2_MOUSE	P08206 mus muscu
38	81.5	11.0	782	1 IP2_MOUSE	P08206 mus muscu
39	81	10.9	100	1 S11_HUMAN	P08206 mus muscu
40	81	10.9	112	1 S10A_MOUSE	P31725 mus muscu
41	80.5	10.9	1013	1 A60D_MOUSE	P31927 drosophila
42	80.5	10.9	2493	1 YBA4_YEAST	P35194 saccharomyc
43	80	10.8	1333	1 SC01_SCHPO	P08206 mus muscu
44	79.5	10.7	93	1 S105_MOUSE	P08206 mus muscu
45	79.5	10.7	99	1 S11_PIG	P31950 sus scrofa

ALIGNMENTS

RESULT 1
ID S10A_RAT STANDARD; PRT; 93 AA.
AC P35467;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE S-100 protein, alpha chain.
GN S100A1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Song W.;
RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 10-93 FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=92076235; PubMed=1742602;
RA Zimmer D.B.; Song W.; Zimmer W.E.;
RT "Isolation of a rat S100 alpha cDNA and distribution of its mRNA in rat tissues."
CC Brain Res. Bull. 27:157-162(1991).
CC -1- FUNCTION: Weakly binds calcium but binds zinc very tightly-
CC distinct binding sites with different affinities exist for both
CC ions on each monomer. Physiological concentrations of potassium
CC affecting high-affinity calcium-binding sites.
CC -1- SUBUNIT: Dimer of either two alpha chains, or two beta chains, or
CC one alpha and one beta chain.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Although predominant among the water-soluble
CC brain proteins, S-100 is also found in a variety of other tissues.
CC -1- SIMILARITY: Belongs to the S-100 family.
CC -1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U26358; AAB3657.1; -
CC EMBL; U26357; AAB53657.1; JOINED.
CC EMBL; S68809; AAB20539.2; -
CC PDB; 1K2H; 13-FEB-02.
CC InterPro; IPR001751; CAP S100.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; EF-hand; 1.
CC Pfam; PF01023; S_100; 1.
CC ProDom; PD003407; Cap_S100; 1.

DR PRODOM: PD000012; EF-hand; 1.
 DR PROSITE; PS00018; EF HAND; 1.
 DR PROSITE; PS00303; S100_CABP; 1.
 KM Calcium-binding; zinc; Metal-binding; 3D-structure.
 FT INT_MET 0
 FT CA_BIND 19 32 EF-HAND 1 (LOW AFFINITY).
 FT CA_BIND 62 73 EF-HAND 2 (HIGH AFFINITY).
 FT CONFLICT 13 13 N -> H (IN REF. 2).
 FT CONFLICT 56 56 K -> R (IN REF. 2).
 SQ SEQUENCE 93 AA; 10429 MW; D2959A95SEC0651A9 CRC64;
 Query Match 18.7%; Score 138.5; DB 1; Length 93;
 Best Local Similarity 36.6%; Pred. No. 1.8e-05;
 Matches 30; Conservative 21; Mismatches 28; Indels 3; Gaps 1;
 QY 54 SDEKAIATATLALFRNSSDSG--KLEKAIANDLQTOFRNFAEGETKPKYRIISL 110
 DB 2 SELESMETLINVFHAGSGEGDKYKSKELKDLQITLSFLDVQADAVDKIMEL 61
 QY 111 DEHTENKLDPEDEFMILLSTIV 132
 DB 62 DENGDEGVDFEYVVAALTV 83
 RESULT 2
 S10A_MOUSE STANDARD; PRT; 93 AA.
 AC P56565; O88949; Rel. 37, Created
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE S-100 protein, alpha chain (S100 calcium-binding protein A1).
 GN S100A1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
 RA Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
 RA Schellenberg K., Stepien M., Tan F., Underwood K., Moore B.,
 RA Theisinger B., Wylie T., Lennon G., Soares B., Wilson R., Waterston R.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99117144; PubMed=9920416;
 RA Ridinger K., Ilg E.C., Niggli F.R., Heizmann C.W., Schaefer B.W.;
 RT "Clustered organization of S100 genes in human and mouse";
 RL Biochem. Biophys. Acta 1448:254-263(1998).
 CC -!- FUNCTION: Weakly binds calcium but binds zinc very tightly-
 distinct binding sites with different affinities exist for both
 ions on each monomer. Physiological concentrations of potassium
 ion antagonize the binding of both divalent cations, especially
 affecting high-affinity calcium-binding sites (by similarity).
 CC -!- SUBUNIT: Dimer of either two alpha chains, or two beta chains, or
 one alpha and one beta chain (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the S-100 family.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; AA000715; -; NOT_ANNOTATED_CDS.
 DR EMBL; AA207748; -; NOT_ANNOTATED_CDS.
 DR EMBL; AA500563; -; NOT_ANNOTATED_CDS.
 DR EMBL; AA432539; -; NOT_ANNOTATED_CDS.

DR EMBL; AF087687; AAC64108.1; -.
 DR HSSP; P04631; 1BAC.
 DR MGD; MG11338917; S100a1.
 DR InterPro; IPR001751; CABP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ethand; 1.
 DR Pfam; PF01023; S100; 1.
 DR PRODOM; PD003407; CABP_S100; 1.
 DR PRODOM; PD000012; EF-hand; 1.
 DR PROSITE; PS00018; EF HAND; 1.
 DR PROSITE; PS00303; S100_CABP; 1.
 KM Calcium-binding; zinc; Metal-binding.
 FT INT_MET 0
 FT CA_BIND 19 32 EF-HAND 1 (LOW AFFINITY) (BY SIMILARITY).
 FT CA_BIND 62 73 EF-HAND 2 (HIGH AFFINITY) (BY SIMILARITY).
 FT CONFLICT 21 21 Q -> E (IN AA207749).
 FT CONFLICT 21 21 Q -> M (IN AA500563).
 FT CONFLICT 21 21 Q -> H (IN AA432539).
 FT CONFLICT 21 21 Q -> K (IN REF. 2).
 SQ SEQUENCE 93 AA; 10374 MW; C969E39E18D705C CRC64;
 Query Match 18.0%; Score 133.5; DB 1; Length 93;
 Best Local Similarity 34.1%; Pred. No. 4.8e-05;
 Matches 28; Conservative 22; Mismatches 29; Indels 3; Gaps 1;
 QY 54 SDEKAIATATLALFRNSSDSG--KLEKAIANDLQTOFRNFAEGETKPKYRIISL 110
 DB 2 SELESMETLINVFHAGSGEGDKYKSKELKDLQITLSFLDVQADAVDKIMEL 61
 QY 111 DEHTENKLDPEDEFMILLSTIV 132
 DB 62 DENGDEGVDFEYVVAALTV 83
 RESULT 3
 S10A_BOVIN STANDARD; PRT; 93 AA.
 AC P02639; Rel. 01, Created
 DT 21-JUN-1986 (Rel. 01, Last sequence update)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE S-100 protein, alpha chain.
 GN S100A1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=66248083; PubMed=3755105;
 RA Kuwano R., Meedi T., Usui H., Arai K., Yamakuni T., Ohshima Y.,
 RA Kurihara T., Takahashi Y.;
 RT "Molecular cloning of cDNA of S100 alpha subunit mRNA";
 RL FEBS Lett. 202:97-101(1986).
 [2]
 RP SEQUENCE.
 RX MEDLINE=81236562; PubMed=7250124;
 RA Isebe T., Okuyama T.;
 RT "The amino-acid sequence of the alpha subunit in bovine brain S-100a
 protein";
 RL Eur. J. Biochem. 116:79-86(1981).
 [3]
 RN METAL ION-BINDING PROPERTIES.
 RP MEDLINE=84000339; PubMed=6615778;
 RA Baudier J., Gerard D.;
 RT "Ions binding to S100 proteins: structural changes induced by calcium
 and zinc on S100a and S100b proteins";
 RL Biochemistry 22:3360-3369(1983).
 CC -!- FUNCTION: Weakly binds calcium but binds zinc very tightly-
 distinct binding sites with different affinities exist for both
 ions on each monomer. Physiological concentrations of potassium

```

CC ion antagonize the binding of both divalent cations, especially
CC affecting high-affinity calcium-binding sites.
CC -1- SUBUNIT: Dimer of either two alpha chains, or two beta chains, or
CC one alpha and one beta chain.
CC -1- TISSUE SPECIFICITY: Although predominant among the water-soluble
CC brain proteins, S-100 is also found in a variety of other tissues.
CC -1- SIMILARITY: Belongs to the S-100 family.
CC PIR: A24156; BCB01A.
DR HSP; P04631; I94C.
DR InterPro: IPR001751; CABP_S100.
DR InterPro: IPR02048; EF-hand.
DR Pfam: PF00036; ehand; 1.
DR Pfam: PF01023; S_100; 1.
DR ProDom: PD003407; CABP_S100; 1.
DR PROSITE: PS00018; EF_HAND; 1.
DR PROSITE: PS00303; S100_CABP; 1.
DR Calcium-binding; Zinc; Metal-binding.
KM INIT MET 0
FT MOD_RES 1 BLOCKED.
FT CA_BIND 19 EF_HAND 1 (LOW AFFINITY).
FT CA_BIND 62 EF_HAND 2 (HIGH AFFINITY).
FT CONFLICT 64 N -> D (IN REF. 2).
SQ SEQUENCE 93 AA; 10387 MW; 0457D0F44819B89B CRC64;

Query Match 17.9%; Score 132.5; DB 1; Length 93;
Best Local Similarity 32.9%; Pred. No. 5.9e-05;
Matches 27; Conservative 23; Mismatches 29; Indels 3; Gaps 1;

CY 54 SDLEKATATLIFRNSSDSG--KLEKAIADLDTQFRNPAEGGTCKPKREILSEL 110
DB 2 SELEFAMETLINVFAHSGKGDYKSKKEIKELDTLSGFLDAGQDAVDKVKEL 61
DB 62 DENGDEVDFOEYVVALV 83

111 DEHTENKLPDEFEMILLISTIV 132
DB 62 DENGDEVDFOEYVVALV 83

RESULT 4
ID S10A HUMAN STANDARD; PRT; 93 AA.
AC P23357;
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DR S-100 protein, alpha chain (S100 calcium-binding protein A1).
DR S100A1 OR S100A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RC MEDLINE=93041710; PubMed=1384693;
RA Engelkamp D., Schaefer B.W., Erne P., Heizmann C.W.;
RT "S100 alpha, CAP1, and CACY: molecular cloning and expression
RT analysis of three calcium-binding proteins from human heart.";
RL Biochemistry 31:10258-10264(1992).

RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Pelting E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.F., Wang T., Hsieh F.,
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong J.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cassavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uebin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Miliaty S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RA Villalon D.K., Wazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Weakly binds calcium but binds zinc very tightly-
CC distinct binding sites with different affinities exist for both
CC ions on each monomer. Physiological concentrations of potassium
CC ion antagonize the binding of both divalent cations, especially
CC affecting high-affinity calcium-binding sites.
CC -1- SUBUNIT: Dimer of either two alpha chains, or two beta chains, or
CC one alpha and one beta chain.
CC -1- SUBCELLULAR LOCATION: Highly prevalent in heart. Also found in
CC lesser quantities in skeletal muscle and brain.
CC -1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL: X58079; CA41107.1; -.
DR EMBL: BC014392; AAH14392.1; -.
DR PIR: A44470; BCB01A.
DR HSP; P04631; I94C.
DR Genew; HGNC:10486; S100A1.
DR MIM; 176940; -.
DR GO; GO:0005509; F:calcium ion binding; NMS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0008270; F:zinc ion binding; NMS.
DR InterPro: IPR001751; CABP_S100.
DR InterPro: IPR02048; EF-hand.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CABP_S100; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
DR Calcium-binding; Zinc; Metal-binding.
KM INIT MET 0 BY SIMILARITY.
FT CA_BIND 19 EF_HAND 1 (LOW AFFINITY).
FT CA_BIND 62 EF_HAND 2 (HIGH AFFINITY).
SQ SEQUENCE 93 AA; 10415 MW; 0457C356C22B899 CRC64;

Query Match 17.7%; Score 131.5; DB 1; Length 93;
Best Local Similarity 32.9%; Pred. No. 7.2e-05;
Matches 27; Conservative 22; Mismatches 29; Indels 3; Gaps 1;

CY 54 SDLEKATATLIFRNSSDSG--KLEKAIADLDTQFRNPAEGGTCKPKREILSEL 110
DB 2 SELEFAMETLINVFAHSGKGDYKSKKEIKELDTLSGFLDAGQDAVDKVKEL 61
DB 62 DENGDEVDFOEYVVALV 83

111 DEHTENKLPDEFEMILLISTIV 132
DB 62 DENGDEVDFOEYVVALV 83

RESULT 5
ID S102 HUMAN STANDARD; PRT; 97 AA.
AC P29034; CO0266; Q9R883;
DT 01-DEC-1992 (Rel. 24, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

```

DE S100 calcium-binding protein A2 (S-100L protein) (CAN19).
GN S100A2 OR S100L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92196147; PubMed=1372446;
RA Lee S.W., Tomasetto C., Swisshelm K., Keyomarsi K., Sager R.;
RT "Down-regulation of a member of the S100 gene family in mammary
RT carcinoma cells and reexpression by azidothymidine treatment.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2504-2508(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96142474; PubMed=9481475;
RA Wicki R., Franz C., Scholl F.A., Heizmann C.W., Schaefer B.W.;
RT "Repression of the candidate tumor suppressor gene S100A2 in breast
RT cancer is mediated by site-specific hypermethylation.";
RL Cell Calcium 22:243-254(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Murnisin K., Farmer A.A., Rubin G.M., Hong L.,
RA Stacheron M., Soares M.B., Bonaldo M.F., Casavant T.E.,
RA Brownstein W.J., Ustin T.B., Toshimori S., Cantucci P., Prange C.,
RA Rana S.S., Loughell N.A., Peters G.J., Adamson R.D., Mullany S.J.,
RA Bosak S.A., McKeown P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Abbey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonfield G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Smalins D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 36-39 AND 41-46.
RX TISSUE-Keratinocytes; PubMed=1286667;
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.R., Van Damme T., Puype M., Geeser B., Celis J.E.,
RA Vandekeizerhoef J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969(1992).
CC -I- FUNCTION: May act as a modulator against excess calcium
CC accumulation in normal human mammary epithelial cells. May also
CC play a role in suppressing tumor cell growth.
CC -I- TISSUE SPECIFICITY: A subset of epithelial cells amongst which
CC normal human mammary epithelial cells and keratinocytes.
CC -I- DEVELOPMENTAL STAGE: Preferentially expressed in normal human
CC mammary epithelial cells as opposed to tumor-derived ones. The
CC level of S100L was shown to correlate inversely with tumor
CC progression.
CC -I- INDUCTION: By growth factors in early G1 phase and probably by
CC cell-cycle regulation in S phase. DNA methylation probably plays
CC a direct negative role in suppressing S100L gene expression in
CC tumor cells.
CC -I- MISCELLANEOUS: This protein binds two calcium ions (By
CC similarity).
CC -I- SIMILARITY: Belongs to the S-100 family.
CC -I- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -

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CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@sb-sib.ch).
CC -----
CC EMBL; M87068; NOT ANNOTATED_CDS.
CC EMBL; Y07755; CA65033.1; --
CC EMBL; BC002829; AA02829.2; --
CC HSSP; P30801; 1A03.
CC Aarhu/Ghent-2DPAGE; 9027; IEF.
CC Aarhu/Ghent-2DPAGE; 9051; IEF.
CC Genew; HGNC:10492; S100A2.
CC MIM; 176993;
CC GO; GO:0005509; F:calcium ion binding; NAS.
CC InterPro; IPR001751; CABP_S100.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF01023; S_100; 1.
CC ProDom; PD003407; CABP_S100; 1.
CC ProDom; PD000012; EF-hand; 1.
CC ProSite; PS00018; EF-HAND; 1.
CC ProSite; PS00303; S100_CABP; 1.
CC KEGG; K04420; S100_CABP; 1.
CC CA_BIND; 20
CC CA_BIND; 63
CC CA_BIND; 61
CC CONFLICT; 61
CC SEQUENCE; 97 AA; 10986 MW; CFB06CD8D0C08D250 CRC64;
CC
CC Query Match 16.6%; Score 123; DB 1; Length 97;
CC Best Local Similarity 31.1%; Pred. No. 0.00041;
CC Matches 28; Conservative 22; Mismatches 36; Indels 4; Gaps 2;
CC
CC QY 53 CSIDLKATATTAIFRNSDSG--KLEKAIKDLQTFQNFAGQETKRRRLISE 109
CC DB 2 CSSLSEGLAVLVTFYKYSQEDKPKLKGEMKELHREKLPFVGEKVDGLKMGWS 61
CC QY 110 IDEHTEKRLDFEDFMILSIYTW-SDLLQ 138
CC DB 62 LDENSDDQVDFQRYAVFLALITVCMDFDQ 91
CC
CC RESULT 6
CC ID S102 BOVIN STANDARD; PRT; 97 AA.
CC AC P10462;
CC DT 01-JUN-1989 (Rel. 11, Created)
CC DT 01-JUN-1989 (Rel. 11, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE S100 calcium-binding protein A2 (S-100L protein).
CC GN Bos taurus (Bovine).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC OC Bovidae; Bovinae; Bos.
CC OX NCBI_TaxID=9913;
CC RN [1]
CC RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
CC RX TISSUE=Lung; PubMed=2521861;
CC RX MEDLINE=89139574; PubMed=2521861;
CC RA Glenney J.R., Jr., Kindy M.S., Zokas L.;
CC RT "Isolation of a new member of the S100 protein family: amino acid
CC sequence, tissue, and subcellular distribution.";
CC RL J. Cell Biol. 108:569-578(1989).
CC -I- SUBUNIT: Homomultimeric (Probable).
CC -I- MISCELLANEOUS: This protein binds two calcium ions.
CC -I- SIMILARITY: Belongs to the S-100 family.
CC -I- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC PIR; A30129; A30129.
CC HSRP; P30801; 1A03.
CC InterPro; IPR001751; CABP_S100.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF01023; S_100; 1.
CC ProDom; PD003407; CABP_S100; 1.
CC ProDom; PD000012; EF-hand; 1.

DR PRODOM, PD000012; EF-hand; 1.
 DR PROSITE, PS00018; EF_HAND; 1.
 DR PROSITE, PS00303; S100_CABP; 1.
 KW Calcium-binding.
 FT CA BIND 20 EF-HAND 1 (LOW AFFINITY) (POTENTIAL).
 FT CA BIND 63 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).
 SQ SEQUENCE 97 AA; 10893 MW; 55ACCF60CF9CBE6 CRC64;
 Query Match 15.7%; Score 116; DB 1; Length 97;
 Best Local Similarity 29.2%; Pred. No. 0.0016;
 Matches 26; Conservative 24; Mismatches 35; Indels 4; Gaps 2;
 QY 54 SDLEKAVITTLIFNSSSDSG---KLEKAIAKDLQTFQFPAEGQETPKYREILSEL 110
 DB 3 SPLEQALVAVMTATFKYSGQEGDKRLKSGEKELHLELPSFVGEKXDEGLKKMGDL 62
 QY 111 DEHTENKLDPEDEPMILLISITVM-SDLIQ 138
 DB 63 DENSQOVDFOEYAVFALITIMCNDPFO 91
 RESULT 7
 ID S104_HUMAN STANDARD; PRT; 101 AA.
 AC P26447;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Placental calcium-binding protein (Calvesculin) (S100 calcium-binding protein A4) (MTS1 protein).
 GN S100A4 OR CAPL OR MTS1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Heart;
 RX MEDLINE=93041710; PubMed=1384693;
 RA Engelkamp D., Schaefer B.W., Erne P., Heizmann C.W.;
 RT "S100 alpha, CAPL, and CACY: molecular cloning and expression analysis of three calcium-binding proteins from human heart.";
 RL Biochemistry 31:10258-10264(1992).
 RN [2]
 RC SEQUENCE FROM N.A.
 RX MEDLINE=93342029; PubMed=8341667;
 RA Engelkamp D., Schaefer B., Mattei M.-G., Erne P., Heizmann C.W.;
 RT "Six S100 genes are clustered on human chromosome 1921: identification of two genes coding for the two previously unreported calcium-binding proteins S100D and S100E.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:6547-6551(1993).
 RN [3]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Spleen;
 RX MEDLINE=93028421; PubMed=1329089;
 RA Tsuchinsky E.M., Ford H.L., Kramarov D., Reshetnyak E., Grigorian M., Zain S., Jukandin E.;
 RT "Transcriptional analysis of the mts1 gene with specific reference to 5' flanking sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:9146-9150(1992).
 RN [4]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Cervix, and Prostate;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D., Altshuler S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marisla K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz J.E., Brownstein M.J., Uudin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullan S.J., Bosak S.A., McEwan P.D., McKernan K.J., Malek J.A., Gunaratne P.R.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Rhee J., Helton E., Ketterman M., Madao A., Rodriguez S., Sanchez A., Whiting M., Madao A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schultz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- TISSUE SPECIFICITY: Ubiquitously expressed.
 CC -1- SIMILARITY: Belongs to the S-100 family.
 CC -1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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 CC
 CC EMBL, M90563; AA51920.1; -;
 CC EMBL, Z18950; CA79474.1; -;
 CC EMBL, Z13457; CA83880.1; -;
 CC EMBL, BC000838; AA00838.1; -;
 CC EMBL, BC016300; AA016300.1; -;
 CC PIR, A48219; A48219.
 CC PDB, 1M31; 3O-OCT-02.
 CC SWISS-2DPAGE, P26447; HUMAN.
 CC Genew, HGNC:10494; S100A4.
 CC MIM, 114210; -;
 CC DR GO, GO:0005509; F:calcium ion binding; TAS.
 CC DR InterPro, IPR001751; CAPL S100.
 CC DR InterPro, IPR02048; EF-hand.
 CC Pfam, PF00036; ehand; 1.
 CC Pfam, PF01023; S_100; 1.
 CC PRODOM, PD003407; CAPL S100; 1.
 CC PRODOM, PD000012; EF-hand; 1.
 CC PROSITE, PS00018; EF_HAND; 1.
 CC PROSITE, PS00303; S100_CABP; 1.
 KW Calcium-binding; 3D-structure.
 FT CA BIND 20 EF-HAND 1 (LOW AFFINITY) (POTENTIAL).
 FT CA BIND 63 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).
 SQ SEQUENCE 101 AA; 11728 MW; 286D2B7B07EB562 CRC64;
 Query Match 14.4%; Score 106.5; DB 1; Length 101;
 Best Local Similarity 28.4%; Pred. No. 0.011;
 Matches 23; Conservative 22; Mismatches 33; Indels 3; Gaps 1;
 QY 56 LEXKATATLIFNSSSDSG---KLEKAIAKDLQTFQFPAEGQETPKYREILSEL 112
 DB 5 LEXALDVAVSTFKYSGQEGDKRLKSGEKELHLELPSFVGEKXDEGLKKMGDL 64
 QY 113 HTENKLDPEDEPMILLISITVM 133
 DB 65 NRDNVDVDFQECVFLSCIAMM 85
 RESULT 8
 ID S10B_MOUSE STANDARD; PRT; 91 AA.
 AC P50114;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE S-100 protein; Beta chain.
 GN S100B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 NCBI_TaxId=10090;

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Db 1 SERIERKVVALLIDVFHFQYSGREDDKTKKSEIKELINNELSHFLBEIKQEVVDMKMTL
Qy 111 DEHTENKLDPEDEFMILLISIT 131
Db 61 DEDGDGCDCEQEFMAFVAMVMT 81

RESULT 9
ID S10B RAT STANDARD; PRT; 91 AA.
S10B RAT
AC P04631;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE S-100 protein, beta chain.
GN S100B.
OC Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteleia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_Taxid=10116;
[1]
SEQUENCE FROM N.A.
MEDLINE=685037924; PubMed=6093041;
Kuwano R., Usui H., Maeda T., Fukui T., Yamamori N., Ohtsuka E.,
Ikahara M., Takahashi Y.,
"Genomic cloning and the complete nucleotide sequence of cDNA to
mRNA for S-100 protein of rat brain."
Nucleic Acids Res. 12:7455-7465(1984).
[2]
SEQUENCE FROM N.A.
Kuwano R., Usui H., Maeda T., Araki K., Kurihara T., Yamakuni T.,
Ohtsuka E., Ikahara M., Takahashi Y.,
"Genomic cloning and nucleotide sequences of cDNA and genomic DNA
for alpha and beta subunits of S100 protein."
Taniguchi Symp. Brain Sci. 19:243-255(1987).
[3]
SEQUENCE FROM N.A.
MEDLINE=91359841; PubMed=1653368;
Maeda T., Usui H., Araki K., Kuwano R., Takahashi Y., Suzuki Y.,
"Structure and expression of rat S-100 beta subunit gene."
Brain Res. Mol. Brain Res. 10:193-202(1991).
[4]
SEQUENCE OF 5-91 FROM N.A.
MEDLINE=87137648; PubMed=3818655;
Dunn R., Landry C., O'Hanlon D., Dunn J., Allore R., Brown I.,
Marx A.,
"Reduction in S100 protein beta subunit mRNA in C6 rat glioma cells
following treatment with anti-microtubular drugs."
J. Biol. Chem. 262:3562-3566(1987).
[5]
STRUCTURE BY NMR.
MEDLINE=963687197; PubMed=8794373;
Drohat A.C., Amburgey J.C., Abildgaard F., Starich M.R.,
Baldisserti D.M., Weber D.J.,
"Solution structure of rat apo-S100B(beta beta) as determined by NMR
spectroscopy."
Biochemistry 35:11577-11588(1996).
[6]
STRUCTURE BY NMR.
MEDLINE=981553156; PubMed=9485423;
Drohat A.C., Baldisserti D.M., Rustandi R.R., Weber D.J.,
"Solution structure of calcium-bound rat S100B(beta beta) as
determined by nuclear magnetic resonance spectroscopy."
Biochemistry 37:2729-2740(1998).
[7]
STRUCTURE BY NMR.
MEDLINE=99226808; PubMed=10211826;
Drohat A.C., Tjandra N., Baldisserti D.M., Weber D.J.,
"The use of dipolar couplings for determining the solution structure
of rat apo-S100B."
Protein Sci. 8:800-809(1999).
-1- FUNCTION: Weakly binds calcium but binds zinc very tightly-

```

DR	EMBL; X01090;	CAA25567.1; -.
DR	EMBL; M54919;	AAA42096.1; -.
DR	EMBL; S53527;	-; NOT_ANNOTATED_CDS.
DR	EMBL; S53522;	-; NOT_ANNOTATED_CDS.
DR	EMBL; M15705;	-; NOT_ANNOTATED_CDS.
PIR	A60046;	A26557.
DR	PDB; 1SYM;	07-DEC-96.
DR	PDB; 1QLK;	11-NOV-98.
DR	PDB; 1B4C;	30-DEC-98.
DR	PDB; 1DT7;	26-JUL-00.
DR	PDB; 1MWI;	18-DEC-02.
DR	GO; GO:0005737;	C:cytoplasm; ISS.
DR	GO; GO:0005575;	C:extracellular; ISS.
DR	GO; GO:0005509;	F:calcium ion binding; ISS.
DR	GO; GO:0019210;	F:kinase inhibitor activity; ISS.
DR	GO; GO:0048156;	F:tau protein binding; ISS.
DR	GO; GO:0008270;	F;zinc ion binding; ISS.
DR	GO; GO:0048143;	F:astrocyte activation; ISS.
DR	GO; GO:0007409;	F:xenogenesis; ISS.
DR	GO; GO:0006877;	F:calcium ion homeostasis; ISS.
DR	GO; GO:0006112;	F:energy reserve metabolism; ISS.
DR	GO; GO:0048151;	F:hyperphosphorylation; ISS.
DR	GO; GO:0006917;	F:induction of apoptosis; ISS.
DR	GO; GO:0007611;	F:learning and/or memory; ISS.
DR	GO; GO:0045917;	F:positive regulation of complement activation; ISS.
DR	GO; GO:0024203;	F:regulation of cytokine biosynthesis; ISS.
DR	GO; GO:0048169;	F:regulation of long-term neuronal synaptic p...; ISS.
DR	GO; GO:0006417;	F:regulation of protein biosynthesis; ISS.
DR	InterPro; IPR001751;	CABP_S100.
DR	InterPro; IPR002048;	EF-hand.
DR	Pfam; PF000036;	efhand; 1.
DR	Pfam; PF01023;	S_100; 1.
DR	ProDom; PD003407;	CABP_S100; 1.
DR	PROSITE; PS00018;	EF_HAND; 1.
DR	PROSITE; PS00303;	S100_CABP; 1.
KW	Calcium-binding;	Zinc; Metal-binding; 3D-structure.
FT	INIT_MET	0
FT	CA_BIND	18 31 EF-HAND 1 (LOW AFFINITY).
FT	CA_BIND	61 72 EF-HAND 2 (HIGH AFFINITY).
FT	HELIX	2 17
FT	TURN	18 19
FT	STRAND	27 27
FT	HELIX	29 39
FT	TURN	41 42
FT	HELIX	43 46
FT	HELIX	50 61
FT	TURN	62 62
FT	STRAND	68 68
FT	HELIX	70 83
FT	TURN	87 88
SEQ	SEQUENCE	91 AA; 10613 MW; 2378AABBF713AD CRC64;

	Query Match	13.8%	Score 102.5	DB 1,	Length 100
--	-------------	-------	-------------	-------	------------

Best Local Similarity 28.4%, Pred. No. 0.025,
Matches 23, Conservative 22, Mismatches 33, Indels 3, Gaps 1,
QY 56 LEKATATLALFRNSDSG---KLEKAIKDLQTOFRNFAEGQETPKYREILSEIDE 112
DB 4 LEKALVWVSTFKHSGKSGDKFKLNSKLKELTRELPSLTGKRTDEAFQKLSNIDC 63
QY 113 HTENKIDFEDFMILLISTVM 133
DB 64 NKDNEVDFOEYCVFLSCIAM 84

RESULT 11
S104_MOUSE STANDARD; PRT; 101 AA.
AC P07091; P20066;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Placental calcium-binding protein (18a2) (PEL98) (MTS1 protein)
DE (metastatic cell protein).
GN S1004 OR CAPL OR MTS1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C;
RX JACKSON-GRUBBY L.L., Swiergiel J., Linzer D.I.H.;
RT "A growth-related mRNA in cultured mouse cells encodes a placental
RT calcium binding protein."
RL Nucleic Acids Res. 15:6677-6690(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C;
RX MEDLINE=8198109; PubMed=3162911;
RA Goto K., Endo H., Fujiyoshi T.;
RT "Cloning of the sequences expressed abundantly in established cell
RT lines: identification of a cDNA clone highly homologous to S-100, a
RT calcium binding protein."
RL J. Biochem. 103:48-53(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89378739; PubMed=2550322;
RA Ebralidze A., Tulchinsky E., Grigorian M., Afanasyeva A., Senin V.,
RA Ravazova E., Lukandin E.;
RT "Isolation and characterization of a gene specifically expressed in
RT different metastatic cells and whose deduced gene product has a high
RT degree of homology to a Ca2+-binding protein family."
RL Genes Dev. 3:1086-1093(1989).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=9023613; PubMed=2332170;
RA Tulchinsky E.M., Grigorian M.S., Ebralidze A.K., Mlishina N.I.,
RA Lukandin E.M.;
RT "Structure of gene mts1, transcribed in metastatic mouse tumor
RT cells."
RL Gene 87:219-223(1990).
RN [5]
RP SEQUENCE OF 1-54 FROM N.A.
RX MEDLINE=93141279; PubMed=8423998;
RA Tulchinsky E., Kramerov D., Ford H.L., Reshetnyak E., Lukandin E.,
RA Zain S.;
RT "Characterization of a positive regulatory element in the mts1 gene."
RL Oncogene 8:79-86(1993).
CC -1- TISSUE SPECIFICITY: Specifically expressed in different metastatic
CC cells.
CC -1- INDUCTION: The mRNA coding for this protein increases in
CC abundance after serum stimulation of quiescent mouse fibroblasts.
CC -1- SIMILARITY: Belongs to the S-100 family.

CC -1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC -----
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CC -----
CC EMBL; X05835; CA229282.1; -
CC EMBL; D00208; BAA00148.1; -
CC EMBL; M36578; AAA39749.1; -
CC EMBL; M36579; AAA39750.1; -
CC EMBL; X16190; CAA34316.1; -
CC EMBL; X16094; CAA34224.1; -
CC PIR; S06207; S06207.
CC HSSP; P30801; 1A03.
CC MGD; MGI:1330282; S100a4.
CC InterPro; IPR001751; CAP_S100.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; ehand; 1.
CC Pfam; PF01023; S_100; 1.
CC ProDom; PD003407; CAP_S100; 1.
CC PROSITE; PS00018; EF_HAND; 1.
CC PROSITE; PS00303; S100_CAP; 1.
CC K1 Calcium-binding; Placenta.
CC CA_BIND 20 33 EF_HAND 1 (LOW AFFINITY) (POTENTIAL);
CC CA_BIND 63 74 EF_HAND 2 (HIGH AFFINITY) (POTENTIAL);
CC CONFLICT 47 47 EF->GVSGSKFNGC (IN REF. 5).
SQ SEQUENCE 101 AA; 11721 MW; 2302254867AFC873 CRC64;
Query Match 13.8%, Score 102.5; DB 1; Length 101;
Best Local Similarity 27.2%, Pred. No. 0.025,
Matches 22, Conservative 22, Mismatches 34, Indels 3, Gaps 1;
QY 56 LEKATATLALFRNSDSG---KLEKAIKDLQTOFRNFAEGQETPKYREILSEIDE 112
DB 5 LEKADLVVSTFKHSGKSGDKFKLNSKLKELTRELPSLTGKRTDEAFQKLSNIDC 64
QY 113 HTENKIDFEDFMILLISTVM 133
DB 65 NKDNEVDFOEYCVFLSCIAM 85

RESULT 12
S109_BOVIN STANDARD; PRT; 122 AA.
AC P28783;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Calgranulin B (Neutrophil cytosolic 23 kDa protein) (P23) (BEE22)
DE (fragment).
GN S100A9.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Esophageal epithelium;
RX MEDLINE=93280230; PubMed=8505358;
RA Tang T.K., Hong T.-M., Lin C.-Y., Lai M.-L., Liu C.H.L., Lo H.-T.,
RA Wang M.-E., Chen L.B., Chen W.-T., Ip W., Lin D.C., Lin J.J.-C.,
RA Lin S., Sun T.-T., Wang E., Wang J.L., Wu R., Wu C.-W., Chien S.;
RT "Nuclear proteins of the bovine esophageal epithelium. I. Monoclonal
RT antibody W2 specifically reacts with condensed nuclei of
RT differentiated superficial cells."
RL J. Cell Sci. 104:237-247(1993).
RN [2]
RP SEQUENCE OF 4-56.

CC TISSUE=Neutrophils;
 RX MEDLINE=92304974; PubMed=1610833;
 RA Dianoou A.-C.; Stasia M.-J.; Garin J.; Gagnon J.; Vignais P.V.;
 RT "The 23-kilodalton protein, a substrate of protein kinase C, in
 RT bovine neutrophil cytosol is a member of the S100 family";
 RL Biochemistry 31:5898-5905(1992).
 CC -1 SUBUNIT: Disulfide linked heterodimer of a 7/11 kDa and a 22/23
 CC kDa subunits.
 CC -1 SUBCELLULAR LOCATION: Cytoplasmic; loosely associated to the
 CC cytoskeleton.
 CC -1 TISSUE SPECIFICITY: Found essentially in phagocytic cells.
 CC -1 PTM: Phosphorylated by protein kinase C.
 CC -1 SIMILARITY: Belongs to the S-100 family.
 CC -1 SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 DR HSP, P80511, 188A.
 DR InterPro; IPR001751; CABP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 1.
 DR Pfam; PF01023; S_100; 1.
 DR Prodom; PD003407; CABP_S100; 1.
 DR Prodom; PD000012; EF-hand; 1.
 DR PROSITE; PS00018; EF_HAND, PARTIAL.
 DR PROSITE; PS00303; S100_CABP; 1.
 KW Calcium-binding; Phosphorylation.
 FT NON_TER 1 1
 FT CA_BIND 19 32 EF_HAND 1 (LOW AFFINITY) (POTENTIAL).
 FT CA_BIND 63 74 EF_HAND 2 (HIGH AFFINITY) (POTENTIAL).
 SQ SEQUENCE 122 AA, 13673 MW, F3CA8C48806BCCD CRC64;
 Query Match 13.8%; Score 102; DB 1; Length 122;
 Best Local Similarity 31.8%; Pred. No. 0.035;
 Matches 27; Conservative 19; Mismatches 35; Indels 4; Gaps 2;
 QY 54 SLEKAIATTAIPNSSDGKLEKAKD--LLQTFRPAFGQ-ETPKREIISE 109
 DB 2 SGMSEIETITITFQYVRGLGHVDTLQKFKQVQKELPKKKQKNAINEIMED 61
 QY 110 IDEHTENKIDFEDFMILLSTVMS 134
 DB 62 LDTNVDKQLSFEEFMTLVRLTVAS 86
 RESULT 13
 S10B_BOVIN STANDARD; PRT; 91 AA.
 AC P02638;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE S-100 protein, beta chain.
 GN S100B.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovine; Bos.
 CX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79045265; PubMed=710399;
 RA "Isobe T., Okuyama T.;
 RT "The amino-acid sequence of S-100 protein (PAP I-b protein) and its
 RT relation to the calcium-binding proteins";
 RL Eur. J. Biochem. 89:379-388(1978).
 RN [2]
 RP REVISIONS TO 1.4.
 RX MEDLINE=81236562; PubMed=7250124;
 RA "Isobe T., Okuyama T.;
 RT "The amino-acid sequence of the alpha subunit in bovine brain S-100a
 RT protein";
 RL Eur. J. Biochem. 116:79-86(1981).
 RN [3]
 RP SEQUENCE.
 RX MEDLINE=855278169; PubMed=4026304;

RA Marshak D.R., Umekawa H., Matterson D.M., Hidaka H.;
 RT "Structural characterization of the calcium binding protein s100 from
 RT adipose tissue.";
 RL Arch. Biochem. Biophys. 240:777-780(1985).
 RP MEDIAL ION-BINDING PROPERTIES.
 RX MEDLINE=84000339; PubMed=6615778;
 RA Buddier J., Gerard D.;
 RT "Ions binding to S100 proteins: structural changes induced by calcium
 RT and zinc on S100a and S100b proteins";
 RL Biochemistry 22:3360-3369(1983).
 RN [5]
 RP CADMIUM-BINDING STUDIES.
 RX MEDLINE=91248136; PubMed=2039467;
 RA Donato H. Jr., Mant R.S., Kay C.M.;
 RT "Spectral studies on the cadmium-ion-binding properties of bovine
 RT brain S-100b protein.";
 RL Biochem. J. 276:13-18(1991).
 RN [6]
 RP STRUCTURE BY NMR.
 RX MEDLINE=96398693; PubMed=8805590;
 RA Kilby P.M., van Eeldik L.J., Roberts G.C.K.;
 RT "The solution structure of the bovine S100B protein dimer in the
 RT calcium-free state.";
 RL Structure 4:1041-1052(1996).
 CC -1 FUNCTION: Weakly binds calcium but binds zinc very tightly-
 CC distinct binding sites with different affinities exist for both
 CC ions on each monomer. Physiological concentrations of potassium
 CC ion antagonize the binding of both divalent cations, especially
 CC affecting high-affinity calcium-binding sites, or two beta chains, or
 CC -1 SUBUNIT: Dimer of either two alpha chains, or two beta chains, or
 CC one alpha and one beta chain.
 CC -1 SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1 TISSUE SPECIFICITY: Although predominant among the water-soluble
 CC brain proteins, S-100 is also found in a variety of other tissues.
 CC -1 SIMILARITY: Belongs to the S-100 family.
 CC -1 SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 DR PIR; A91254; BCB01B.
 DR PDB; 1CFP; 12-MAR-97.
 DR PDB; 1MHO; 18-NOV-98.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005576; C:extracellular; ISS.
 DR GO; GO:0005509; F:calcium ion binding; ISS.
 DR GO; GO:0019240; F:kinase inhibitor activity; NAS.
 DR GO; GO:0042803; F:protein homodimerization activity; ISS.
 DR GO; GO:0048155; F:S100 alpha binding; ISS.
 DR GO; GO:0048154; F:S100 beta binding; ISS.
 DR GO; GO:0048156; F:tau protein binding; IPI.
 DR GO; GO:0008270; F:zinc ion binding; IDA.
 DR GO; GO:0048143; F:astrocyte activation; NAS.
 DR GO; GO:0007409; F:exonogenesis; NAS.
 DR GO; GO:0006874; F:calcium ion homeostasis; ISS.
 DR GO; GO:0006112; F:energy reserve metabolism; ISS.
 DR GO; GO:0048151; F:hyperphosphorylation; NAS.
 DR GO; GO:0006917; P:induction of apoptosis; ISS.
 DR GO; GO:0007611; P:learning and/or memory; ISS.
 DR GO; GO:0045917; P:positive regulation of complement activation; NAS.
 DR GO; GO:0048205; P:regulation of cytokine biosynthesis; ISS.
 DR GO; GO:0048159; P:regulation of long-term neuronal synaptic P...; ISS.
 DR GO; GO:0006417; P:regulation of protein biosynthesis; NAS.
 DR InterPro; IPR002048; CABP_S100.
 DR InterPro; IPR001751; CABP_S100.
 DR Pfam; PF00036; ehand; 1.
 DR Pfam; PF01023; S_100; 1.
 DR Prodom; PD003407; CABP_S100; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS00303; S100_CABP; 1.
 KW Calcium-binding; Zinc; Metal; Metal-binding; Acetylation; 3D-structure.
 FT MOD_RES 1 1
 FT CA_BIND 18 31 ACETYLATION.
 FT CA_BIND 61 72 EF_HAND 1 (LOW AFFINITY).
 FT HELIX 2 18 EF_HAND 2 (HIGH AFFINITY).
 FT TURN 19 19

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FT TURN 24 25
FT STRAND 27 27
FT HELIX 29 39
FT TURN 41 43
FT HELIX 50 60
FT STRAND 68 68
FT HELIX 70 87
SQ SEQUENCE 91 AA; 10537 MW; 386201933DE6B93A CRC64;

Query Match
Best Local Similarity 28.4%; Pred No. 0.027; DB 1; Length 91;
Matches 23; Conservative 20; Mismatches 35; Indels 3; Gaps 1;

QY 54 SLEKAIATTAIFRNSSDSG--KLEKAIKDLQTFNFAEGQETKREIISLSE 110
DB 1 SLEKAVVALIVFHQYSGREGDKHKKSEIKELINNELSHLEIEIKGEVVDKWMETL 60
QY 111 DEHTENKLDPEDEPMILLISIT 131
DB 61 DSDGDECDFOEFMAFVAMIT 81
Db

RESULT 14
S104 RAT STANDARD; PRT; 101 AA.
AC P05942;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Placental calcium-binding protein (Nerve growth factor induced protein 42A) (99K).
GN S100A4
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88118907; PubMed=3422491;
RA Maslakowski P., Shooter E.M., the genes for two proteins related to a
RT Nerve growth factor induces the genes for two proteins related to a
RT family of calcium-binding proteins in PC12 cells."
RT Proc. Natl. Acad. Sci. U.S.A. 85:1277-1281 (1988).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88118907; PubMed=3430604;
RA Barricough R., Savin J., Dube S.K., Rudland P.S.,
RT Molecular cloning and sequence of the gene for p9Ka, a cultured
RT myoepithelial cell protein with strong homology to S-100, a calcium-
RT binding protein."
RT J. Mol. Biol. 198:13-20 (1987).
[3]
RP SEQUENCE OF 3-101 FROM N.A.
RX MEDLINE=92158347; PubMed=1741158;
RA de Vonge M.W., Mukherjee B.B.,
RT Transformation of normal rat kidney cells by v-K-ras enhances
RT expression of transin 2 and an S-100-related calcium-binding
RT protein."
RT Oncogene 7:109-119 (1992).
CC -1- INDUCTION: By nerve growth factor.
CC -1- SIMILARITY: Belongs to the S-100 family.
CC -1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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CC
CC EMBL; X06916; CAA30014.1; -
CC
CC EMBL; J03628; AAA42098.1; -

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DR EMBL; X64022; -; NOT ANNOTATED CDS.
DR EMBL; X64023; -; NOT ANNOTATED CDS.
DR PIR; S01759; S01759.
DR HSSP; P30801; 1A03.
DR InterPro; IPR001751; CABP_S100.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 1.
DR ProDom; PD003407; CABP_S100; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding.
FT CA BIND 63 74
FT CA BIND 20 74
SQ SEQUENCE 101 AA; 11776 MW; EA0619CEBA4F487C1 CRC64;

Query Match
Best Local Similarity 25.9%; Pred. No. 0.046; DB 1; Length 101;
Matches 21; Conservative 24; Mismatches 33; Indels 3; Gaps 1;

QY 56 LKKAIAATTAIFRNSSDSG--KLEKAIKDLQTFNFAEGQETKREIISLSE 112
DB 5 LKRALDVIVSTFHRYSGNEGDKFKLNKTEIKELITRELPFLGRTRDEAFAQIMNLD 64
QY 113 HTENKLDPEDEPMILLISITVM 133
DB 65 NRDEVDFOERYCVFLSCIAVM 85
Db

RESULT 15
S10B HUMAN STANDARD; PRT; 91 AA.
AC P04271;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE S-100 protein, beta chain.
GN S100B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
[1]
RP SEQUENCE.
RX MEDLINE=85291729; PubMed=4031854;
RA Jensen R., Marshak D.R., Anderson C., Lukas T.J., Watterson D.M.;
RT "Characterization of human brain S100 protein fraction: amino acid
RT sequence of S100 beta."
RT J. Neurochem. 45:700-705 (1985).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90368757; PubMed=2394738;
RA Allore R.J., Friend W.C., O'Hanlon D., Neilson K.M., Baunat R.,
RA Dunn R.J., Marks A.;
RT "Cloning and expression of the human S100 beta gene."
RT J. Biol. Chem. 265:15537-15543 (1990).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
RA Datchenko L., Marzina K., Farmer A.A., Rubin G.M., Hong D.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E.,
RA Brownstein M.J., Uesdin T.B., Toshitsuki S., Camarini P., Prange C.,
RA Rana S.S., Loguellianno N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Guarnarene P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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OM protein - protein search, using sw model

Run on: June 3, 2004, 13:21:57 ; Search time 44 Seconds
(without alignments)
939.927 Million cell updates/sec

Title: US-09-744-197-1
Perfect score: 741
Sequence: 1 MGCNHSQDKSLHLEDPN.....LSITVMSDLLQINRVKIMK 147

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US03_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	690	93.1	140	9	US-09-764-864-1447
2	131.5	17.7	94	14	US-10-097-340-270
3	123	16.6	97	14	US-10-097-340-274
4	123	16.6	97	14	US-10-171-311-206
5	123	16.6	97	15	US-10-236-031B-40
6	108.5	14.6	134	10	US-09-992-600A-2
7	108.5	14.6	134	10	US-09-924-340-2
8	108.5	14.6	134	10	US-09-992-095B-2
9	108.5	14.6	134	10	US-09-999-570-2
10	108.5	14.6	134	14	US-10-000-489-2
11	108.5	14.6	134	14	US-10-000-986-2
12	108.5	14.6	134	14	US-10-154-678-2
13	106.5	14.4	101	9	US-09-393-433-1
14	106.5	14.4	101	9	US-09-781-509-1
15	106.5	14.4	101	12	US-10-087-192-1158

16	106.5	14.4	101	13	US-10-067-618-2
17	106.5	14.4	101	13	US-10-135-152-2
18	106.5	14.4	101	14	US-10-269-643-1
19	106.5	14.4	134	9	US-09-925-302-694
20	106.5	14.4	134	12	US-09-925-302-694
21	105.5	14.2	119	12	US-10-087-192-1155
22	103	13.9	186	15	US-10-264-049-4104
23	102.5	13.8	101	9	US-09-393-433-2
24	102.5	13.8	101	9	US-09-781-509-2
25	102.5	13.8	101	14	US-10-269-643-2
26	100	13.5	118	15	US-10-264-049-3289
27	98.5	13.3	92	10	US-09-492-026-5
28	98.5	13.3	92	10	US-09-319-039-184
29	98.5	13.3	92	12	US-10-336-603A-102
30	96	13.0	95	10	US-09-877-843-27
31	96	13.0	96	10	US-09-877-843-25
32	96	13.0	97	11	US-09-877-843-26
33	96	13.0	97	11	US-09-997-003-32
34	96	13.0	97	14	US-10-304-287-3
35	96	13.0	112	14	US-10-205-219-161
36	96	13.0	113	10	US-09-492-026-7
37	95	12.8	97	10	US-09-877-843-29
38	91.5	12.3	89	14	US-10-134-841-1
39	91.5	12.3	218	12	US-10-296-115-772
40	91	12.3	97	10	US-09-877-843-28
41	90.5	12.2	89	14	US-10-316-253-46
42	89.5	12.1	95	9	US-09-919-172-102
43	89.5	12.1	95	9	US-09-981-353-98
44	89.5	12.1	113	12	US-10-276-774-2377
45	89	12.0	93	15	US-10-094-886-58

ALIGNMENTS

RESULT 1
US-09-764-864-1447
; Sequence 1447, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1447
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-1447

Query Match 93.1%; Score 690; DB 9; Length 140;
Best Local Similarity 99.3%; Pred. No. 1.4e-64;
Matches 138; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	9	QDKSLHLEGDPNPSAAPTSTCAPKMPKRRISISIKOLASVKALRKCSDLEKAIATTAIFR	68
DB	2	EDKSLHLEGDPNPSAAPTSTCAPKMPKRRISISIKOLASVKALRKCSDLEKAIATTAIFR	61
QY	69	NSSDSGKLEKAIANDLLQTOFRNFAEQETPKYRIILSELDEHTENKLDFFEDFMILL	128
DB	62	NSSDSGKLEKAIANDLLQTOFRNFAEQETPKYRIILSELDEHTENKLDFFEDFMILL	121
QY	129	SITVMSDLLQINRVKIMK	147
DB	122	SITVMSDLLQINRVKIMK	140

RESULT 2
US-10-097-340-270


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; Sequence 270, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPURU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 270
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-270

Query Match 17.7%; Score 131.5; DB 14; Length 94;
Best Local Similarity 32.3%; Pred. No. 5.1e-06;
Matches 27; Conservative 23; Mismatches 29; Indels 3; Gaps 1;

Qy 54 SDEKAIATTAIFRNSSDG---KLEKAIKDLTQTFRNFAGQETKPKYREILSEL 110
Db 3 SELETAMETLINVFAHSGREGDKYKLSKKELKELIQLTSLGFLDAQKDVAQDKVKMEL 62

Qy 111 DEHTENKLDPEDFMILLISITY 132
Db 63 DENGDEGVDFQIVLVLAATV 84

RESULT 3
US-10-097-340-274
; Sequence 274, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPURU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
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; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 274
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-274

Query Match 16.6%; Score 123; DB 14; Length 97;
Best Local Similarity 31.1%; Pred. No. 4.1e-05;
Matches 28; Conservative 22; Mismatches 36; Indels 4; Gaps 2;

Qy 53 CSDLEKAIATTAIFRNSSDG---KLEKAIKDLTQTFRNFAGQETKPKYREILSEL 109
Db 2 CSSLEQALAVLVTTTFHKYSCQGGKFKLKGKMKELHKLKELPSFVGKVDGKLGKMG 61

Qy 110 DEHTENKLDPEDFMILLISITY-SDLLQ 138
Db 62 LDENSQDVDFQEVAVFLALITVWCNDFFQ 91

RESULT 4
US-10-171-311-206
; Sequence 206, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Ganavapur, Manjula
; APPLICANT: Hoersh, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
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RESULT 8
US-09-992-095B-2
; Sequence 2, Application US/09992095B
; Publication No. US20030157485A1

GENERAL INFORMATION:
APPLICANT: Benjamin, Stephane
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US5.DIV
CURRENT APPLICATION NUMBER: US/09/992,095B
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
SEQ ID NO 2
LENGTH: 134
TYPE: PRT
ORGANISM: Homo sapiens
US-09-992-095B-2

Query Match 14.6%; Score 108.5; DB 10; Length 134;
Best Local Similarity 25.2%; Pred. No. 0.0022;
Matches 27; Conservative 23; Mismatches 52; Indels 5; Gaps 1;

Qy 26 TSTCAPKMPKRISISKQLASVKALRKCSDLKAIATTAIFRNSSDSGKLEKAIADL 85
Db 17 TFSCLPRPRTEPL-----VASTDHTKMPQMEHMETMTFTFKFAGDKGYLTEDLRLV 71

Qy 86 LQTOFRNFAEGQETPKYREILSELDEHTENKLDKDFEDFMILLISITV 132
Db 72 MEKEFFPGFLENQKDLAVDKIMKLDQCRDGKVGQSFPSLIAGLTI 118

RESULT 10
US-10-000-489-2
Sequence 2, Application US/10000489
Publication No. US20030092011A1
GENERAL INFORMATION:
APPLICANT: Benjamin, Stephane
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US6.DIV
CURRENT APPLICATION NUMBER: US/10/000,489
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
SEQ ID NO 2
LENGTH: 134
TYPE: PRT
ORGANISM: Homo sapiens
US-10-000-489-2

Query Match 14.6%; Score 108.5; DB 14; Length 134;
Best Local Similarity 25.2%; Pred. No. 0.0022;
Matches 27; Conservative 23; Mismatches 52; Indels 5; Gaps 1;

Qy 26 TSTCAPKMPKRISISKQLASVKALRKCSDLKAIATTAIFRNSSDSGKLEKAIADL 85
Db 17 TFSCLPRPRTEPL-----VASTDHTKMPQMEHMETMTFTFKFAGDKGYLTEDLRLV 71

Qy 86 LQTOFRNFAEGQETPKYREILSELDEHTENKLDKDFEDFMILLISITV 132
Db 72 MEKEFFPGFLENQKDLAVDKIMKLDQCRDGKVGQSFPSLIAGLTI 118

RESULT 11
US-10-000-986-2
Sequence 2, Application US/10000986
Publication No. US20030096247A1
GENERAL INFORMATION:
APPLICANT: Benjamin, Stephane
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US9.DIV
CURRENT APPLICATION NUMBER: US/10/000,986
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277

GENERAL INFORMATION:
APPLICANT: Benjamin, Stephane
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US5.DIV
CURRENT APPLICATION NUMBER: US/09/992,095B
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
SEQ ID NO 2
LENGTH: 134
TYPE: PRT
ORGANISM: Homo sapiens
US-09-992-095B-2

Query Match 14.6%; Score 108.5; DB 10; Length 134;
Best Local Similarity 25.2%; Pred. No. 0.0022;
Matches 27; Conservative 23; Mismatches 52; Indels 5; Gaps 1;

Qy 26 TSTCAPKMPKRISISKQLASVKALRKCSDLKAIATTAIFRNSSDSGKLEKAIADL 85
Db 17 TFSCLPRPRTEPL-----VASTDHTKMPQMEHMETMTFTFKFAGDKGYLTEDLRLV 71

Qy 86 LQTOFRNFAEGQETPKYREILSELDEHTENKLDKDFEDFMILLISITV 132
Db 72 MEKEFFPGFLENQKDLAVDKIMKLDQCRDGKVGQSFPSLIAGLTI 118

RESULT 9
US-09-999-570-2
Sequence 2, Application US/09999570
Publication No. US20030170628A1
GENERAL INFORMATION:
APPLICANT: Benjamin, Stephane
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: G-091US08DIV
CURRENT APPLICATION NUMBER: US/09/999,570
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
SEQ ID NO 2
LENGTH: 134
TYPE: PRT
ORGANISM: Homo sapiens
US-09-999-570-2

Query Match 14.6%; Score 108.5; DB 10; Length 134;
Best Local Similarity 25.2%; Pred. No. 0.0022;

; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 2
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-986-2

Query Match 14.6%; Score 108.5; DB 14; Length 134;
Best Local Similarity 25.2%; Pred. No. 0.0022;
Matches 27; Conservative 23; Mismatches 52; Indels 5; Gaps 1;
Qy 26 TSTCAPKPKRISIKQLASVKALRKCSDLEKAIATATLIFRNSSDSGKLEKAIKOL 85
Db 17 TFSCLPRPRTEPL-----VASTDHTKMPQSQMEHAMETMTFTFKFAGDKGYLTKEIDLRL 71
Qy 86 LQTOFRNFAEGQETPKPKYREILSELDEHTENKLDDEDPMILLISITV 132
Db 72 MEKEFPGLFNQKQDPLAVDKIMKOLDQCRDQKGVGFQSFSLIAGLTI 118

RESULT 12

US-10-154-678-2
; Sequence 2, Application US/10154678
; Publication No. US20030162186A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephanie
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 182.US1.REG
; CURRENT APPLICATION NUMBER: US/10/154,678
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 2
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-678-2

Query Match 14.6%; Score 108.5; DB 14; Length 134;
Best Local Similarity 25.2%; Pred. No. 0.0022;
Matches 27; Conservative 23; Mismatches 52; Indels 5; Gaps 1;
Qy 26 TSTCAPKPKRISIKQLASVKALRKCSDLEKAIATATLIFRNSSDSGKLEKAIKOL 85
Db 17 TFSCLPRPRTEPL-----VASTDHTKMPQSQMEHAMETMTFTFKFAGDKGYLTKEIDLRL 71
Qy 86 LQTOFRNFAEGQETPKPKYREILSELDEHTENKLDDEDPMILLISITV 132
Db 72 MEKEFPGLFNQKQDPLAVDKIMKOLDQCRDQKGVGFQSFSLIAGLTI 118

RESULT 13

US-09-393-433-1
; Sequence 1, Application US/09393433
; Patent No. US2001001126A1
; GENERAL INFORMATION:

; APPLICANT: Lukanidin, Eugene
; APPLICANT: Bock, Elisabeth M.
; APPLICANT: Berezen, Vladimir
; TITLE OF INVENTION: NEUROGENIC COMPOSITIONS AND METHODS
; FILE REFERENCE: RCT
; CURRENT APPLICATION NUMBER: US/09/393,433
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-393-433-1

Query Match 14.4%; Score 106.5; DB 9; Length 101;
Best Local Similarity 28.4%; Pred. No. 0.0024;
Matches 23; Conservative 22; Mismatches 33; Indels 3; Gaps 1;
Qy 56 LEKAIATATLIFRNSSDSG---KLEKAIKOLLQTOFRNFAEGQETPKPKYREILSELDE 112
Db 5 LEKALDVMVSTFHKYSGEGDKFKLKSSELKELLTRELPSFLGKRTDEAFAQKLSNLD 64
Qy 113 HTENKLDDEDPMILLISITVM 133
Db 65 NRDNEVDFOEYCVFLSCIAMM 85

RESULT 14

US-09-781-509-1
; Sequence 1, Application US/09781509
; Patent No. US20020099010A1
; GENERAL INFORMATION:
; APPLICANT: Lukanidin, Eugene
; APPLICANT: Bock, Elisabeth M.
; APPLICANT: Berezen, Vladimir
; TITLE OF INVENTION: NEUROGENIC COMPOSITIONS AND METHODS
; FILE REFERENCE: RCT
; CURRENT APPLICATION NUMBER: US/09/781,509
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 09/393,433
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-781-509-1

Query Match 14.4%; Score 106.5; DB 9; Length 101;
Best Local Similarity 28.4%; Pred. No. 0.0024;
Matches 23; Conservative 22; Mismatches 33; Indels 3; Gaps 1;
Qy 56 LEKAIATATLIFRNSSDSG---KLEKAIKOLLQTOFRNFAEGQETPKPKYREILSELDE 112
Db 5 LEKALDVMVSTFHKYSGEGDKFKLKSSELKELLTRELPSFLGKRTDEAFAQKLSNLD 64
Qy 113 HTENKLDDEDPMILLISITVM 133
Db 65 NRDNEVDFOEYCVFLSCIAMM 85

RESULT 15

US-10-087-192-1158
; Sequence 1158, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122

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; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1158
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-1158

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Query Match      14.4%; Score 106.5; DB 12; Length 101;
Best Local Similarity 28.4%; Pred. No. 0.0024;
Matches 23; Conservative 22; Mismatches 33; Indels 3; Gaps 1;

QY      56 LEKATATTALIFRNSDSG--KLEKAIADLLQTFRPAEQGQETKPKYREILSELDE 112
Db      5 LEKALDVWVSTPHKYSKGEGDKFKLUNKSELKELLTRELPSFLGKRTDEAFAQKLSNLD 64

QY      113 HTENKLDPEDFMILLISITVM 133
Db      65 NRDNEVDVFOEYCVFLSCIAMM 85

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Search completed: June 3, 2004, 13:27:49
Job time : 45 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 13:19:26 ; Search time 22 Seconds
(without alignments)
344.955 Million cell updates/sec

Title: US-09-744-197-1

Perfect score: 741

Sequence: 1 MGGCMHSTQDKSLHLEDPN.....LSITVMSDLLQIRNVKIMK 147

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.*
- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	741	100.0	147	4	US-09-621-976-7168
2	123	16.6	97	1	US-07-662-198B-2
3	106.5	14.4	101	1	US-08-190-560-2
4	106.5	14.4	101	1	US-08-469-277-2
5	106.5	14.4	101	2	US-08-468-946-2
6	106.5	14.4	101	2	US-08-468-942-2
7	106.5	14.4	101	4	US-09-298-625-2
8	102.5	13.8	92	2	US-09-051-589-1
9	98.5	13.3	91	1	US-07-987-272A-11
10	98.5	13.3	92	2	US-08-918-727-5
11	98.5	13.3	92	3	US-09-203-680A-5
12	96	13.0	95	1	US-07-987-272A-9
13	96	13.0	113	2	US-08-918-727-7
14	96	13.0	113	3	US-09-203-680A-7
15	91.5	12.3	88	1	US-07-987-272A-14
16	91.5	12.3	89	1	US-07-987-272A-12
17	89.5	12.1	95	4	US-09-919-172-102
18	89.5	12.1	95	4	US-09-976-594-467
19	89	12.0	95	4	US-09-399-913-65
20	89	12.0	114	1	US-08-385-241-3
21	89	12.0	114	4	US-09-214-272-4
22	86	11.6	75	1	US-07-987-272A-17
23	83.5	11.3	76	1	US-07-987-272A-12
24	79	10.7	109	1	US-07-987-272A-8
25	77	10.4	1664	1	US-09-599-652-2
26	77	10.4	1664	2	US-08-642-846-2
27	77	10.4	1664	4	US-09-264-604-2

28	76.5	10.3	105	2	US-08-918-727-6	Sequence 6, Appli
29	76.5	10.3	105	3	US-09-205-680A-6	Sequence 6, Appli
30	76	10.3	391	3	US-08-773-731A-5	Sequence 5, Appli
31	74	10.0	196	4	US-09-621-976-5041	Sequence 5041, Ap
32	74	10.0	222	4	US-09-203-258-360	Sequence 360, App
33	74	10.0	311	4	US-09-252-991A-23527	Sequence 23527, A
34	74	10.0	456	1	US-08-464-164-2	Sequence 2, Appli
35	74	10.0	456	1	US-08-338-057-2	Sequence 2, Appli
36	74	10.0	456	2	US-08-668-416-2	Sequence 2, Appli
37	73	9.9	328	4	US-09-252-991A-27822	Sequence 27822, A
38	73	9.9	521	2	US-08-406-855A-19	Sequence 19, Appl
39	73	9.9	521	3	US-09-206-899-19	Sequence 19, Appl
40	73	9.9	699	4	US-09-457-040B-18	Sequence 18, Appl
41	72.5	9.8	1093	3	US-09-315-793-52	Sequence 52, Appl
42	72	9.7	101	1	US-08-469-486-58	Sequence 58, Appl
43	72	9.7	101	2	US-08-469-688-58	Sequence 58, Appl
44	72	9.7	230	4	US-09-252-991A-26110	Sequence 26110, A
45	71.5	9.6	1394	4	US-09-845-917A-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1

US-09-621-976-7168
; Sequence 7168, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 7168
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-7168

Query Match 100.0%; Score 741; DB 4; Length 147;
Best Local Similarity 100.0%; Pred No. 7,6e-73;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGGCMHSTQDKSLHLEDPNPSAAPTSTCAPRMKPRISISKOLASVKALRKCSDEKAI	60
Db	1	MGGCMHSTQDKSLHLEDPNPSAAPTSTCAPRMKPRISISKOLASVKALRKCSDEKAI	60
Qy	61	ATTALIFRNSSDGKLEKAIKDLLOTFRPAEQETPKPYREILSLDHTENKLDIF	120
Db	61	ATTALIFRNSSDGKLEKAIKDLLOTFRPAEQETPKPYREILSLDHTENKLDIF	120
Qy	121	EDFMILLISITVMSDLLQIRNVKIMK	147
Db	121	EDFMILLISITVMSDLLQIRNVKIMK	147

RESULT 2

US-07-662-198B-2
; Sequence 2, Application US/07662198B
; Patent No. 5262528
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; APPLICANT: Lee, Sam W.
; APPLICANT: Tomasetto, Catherine
; TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street

```

; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/662,198B
; FILING DATE: 19910228
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/049001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-662-198B-2

Query Match 16.6%; Score 123; DB 1; Length 97;
Best Local Similarity 31.1%; Pred. No. 5.5e-06;
Matches 28; Conservative 22; Mismatches 36; Indels 4; Gaps 2;

QY 53 CSLEKAIATTAIFRNSSDGD---KLEKAIARDLLQTOFRNFAEQGQTKPKYRIILSE 109
Db 2 CSSLEQALAVLVTTFHKYSGEGDKFKLSKGENKELLHKLPFSVGEKVDEGLKLMGN 61

QY 110 LDEHTENKLPEDFMILLLSITVM-SLLQ 138
Db 62 LDENSQQQVDFQYAVFLALITVNCNDFQ 91

RESULT 3
US-08-130-560-2
; Sequence 2, Application US/08190560
; Patent No. 5798257
; GENERAL INFORMATION:
; APPLICANT: Zain, Sayeeda
; APPLICANT: Lukanidin, Eugene
; TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY
; TITLE OF INVENTION: THE MTS-1 GENE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,560
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,560
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 78792Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-130-560-2

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; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 78792Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-130-560-2

Query Match 14.4%; Score 106.5; DB 1; Length 101;
Best Local Similarity 28.4%; Pred. No. 0.00036;
Matches 23; Conservative 22; Mismatches 33; Indels 3; Gaps 1;

QY 56 LEKAIATTAIFRNSSDGD---KLEKAIARDLLQTOFRNFAEQGQTKPKYRIILSE 112
Db 5 LEKALDVNVSTFHKYSGEGDKFKLSKGENKELLTRELPSFLGKRTDEAAAFQKLMNSLDS 64

QY 113 HTENKLPEDFMILLLSITVM 133
Db 65 NRDNVDVDFQYCVFLSCIAMM 85

RESULT 4
US-08-469-277-2
; Sequence 2, Application US/08469277
; Patent No. 5801142
; GENERAL INFORMATION:
; APPLICANT: Zain, Sayeeda
; APPLICANT: Lukanidin, Eugene
; TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY
; TITLE OF INVENTION: THE MTS-1 GENE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,277
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,560
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 78792Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-277-2

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RESULT 6
 US-08-468-942-2
 ; Sequence 2, Application US/08468942
 ; Patent No. 5965360
 ; GENERAL INFORMATION:
 ; APPLICANT: Zain, Saveeda
 ; APPLICANT: Lukanidin, Eugene
 ; TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY
 ; TITLE OF INVENTION: THE MTS-1 GENE
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; Zip: 11530

STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATON NUMBER: US/08/468,942
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/190,560
FILING DATE: 31-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 78792Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-942-2

RESULT 7
US-09-298-625-2
; Sequence 2, Application US/09298625
; Patent No. 6638504
; GENERAL INFORMATION:
; APPLICANT: Lukanidin, Eugene
; TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY THE MTS-1 GENE
; FILE REFERENCE: 7879YXIII-Z
; CURRENT APPLICATION NUMBER: US/09/298,625
; CURRENT FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 08/468,942
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/190,560
; PRIOR FILING DATE: 1994-01-31

;; PRIOR APPLICATION NUMBER: 07/981,455
;; PRIOR FILING DATE: 1992-11-25
;; PRIOR APPLICATION NUMBER: 07/550,600
;; PRIOR FILING DATE: 1990-07-09
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 101
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-298-625-2

Query Match 14.4%; Score 106.5; DB 4; Length 101;
Best Local Similarity 28.4%; Pred. No. 0.00036;
Matches 23; Conservative 22; Mismatches 33; Indels 3; Gaps 1;

QY 56 LEKAIATATLIFRNSSDSG--KLEKAIADLLQTFQFNFAEGQETPKPKYREILSELDE 112
DB 5 LEKALDVMVSTFKYSGKGDGFKLNKSELKELLRELPSFLGKRTDEAFAFKLMSNLD 64

QY 113 HTENKLDFFEDFMILLISITVM 133
DB 65 NRDNVEDFQYCVFLSCIAMM 85

RESULT 8

US-09-051-589-1
Sequence 1, Application US/09051589

Patent No. 5990080

GENERAL INFORMATION:

APPLICANT: HAGLID, Kenneth G.

TITLE OF INVENTION: USE OF PROTEIN S-100B IN MEDICINES CONTAINING THE

TITLE OF INVENTION: PROTEIN S-100B

FILE REFERENCE: 003300-478

CURRENT APPLICATION NUMBER: US/09/051,589

CURRENT FILING DATE: 1998-04-15

EARLIER APPLICATION NUMBER: SE 9503620-8

EARLIER FILING DATE: 1995-10-17

EARLIER APPLICATION NUMBER: PCT/SE96/01305

EARLIER FILING DATE: 1996-10-15

NUMBER OF SEQ ID NOS: 1

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 92

TYPE: PRT

ORGANISM: Protein S-100b

US-09-051-589-1

Query Match 13.8%; Score 102.5; DB 2; Length 92;
Best Local Similarity 28.4%; Pred. No. 0.00086;
Matches 23; Conservative 21; Mismatches 34; Indels 3; Gaps 1;

QY 54 SDLEKAIATATLIFRNSSDSG--KLEKAIADLLQTFQFNFAEGQETPKPKYREILSEL 110
DB 2 SELEKAMVALIDVFHQVSGREGDKHKLSKSELKELINNELSHFLEBIKEQEVVDKVMETL 61

QY 111 DEHTENKLDFFEDFMILLISIT 131
DB 62 DEDGDGCDFOEFMAFVSWT 82

RESULT 9

US-07-987-272A-11

Sequence 11, Application US/07987272A

Patent No. 5731166

GENERAL INFORMATION:

APPLICANT: Geczy, C., Simpson, R. J. and Lackmann, M

TITLE OF INVENTION: No. 5731166el Chemotactic Factor

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cushman Darby & Cushman

STREET: 1100 New York Avenue, N. W., Ninth Floor, East Tower

CITY: Washington

;; STATE: D. C.
;; COUNTRY: USA
;; ZIP: 20005-3918
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/987,272A
;; FILING DATE: 05-MAR-1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: AU PK 2127
;; FILING DATE: 05-FEB-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: AU PK 4463
;; FILING DATE: 05-SEP-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Brinkman, David W
;; REGISTRATION NUMBER: 20,817
;; REFERENCE/DOCKET NUMBER: DMB/1925/200259
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-861 3000
;; TELEFAX: 202-822 0944
;; TELEX: 6714627 CUSH
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 91 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-07-987-272A-11

Query Match 13.3%; Score 98.5; DB 1; Length 91;
Best Local Similarity 27.2%; Pred. No. 0.0023;
Matches 22; Conservative 21; Mismatches 35; Indels 3; Gaps 1;

QY 54 SDLEKAIATATLIFRNSSDSG--KLEKAIADLLQTFQFNFAEGQETPKPKYREILSEL 110
DB 1 SELEKAMVALIDVFHQVSGREGDKHKLSKSELKELINNELSHFLEBIKEQEVVDKVMETL 60

QY 111 DEHTENKLDFFEDFMILLISIT 131
DB 61 DNDGDGCDFOEFMAFVAMVT 81

RESULT 10
US-08-918-727-5

Sequence 5, Application US/08918727

Patent No. 5849528

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Bandman, Olga

APPLICANT: Corley, Neil C.

APPLICANT: Lal, Preeti

APPLICANT: Shah, Purvi

TITLE OF INVENTION: HUMAN S100 PROTEINS

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

Query Match 13.3%; Score 98.5; DB 3; Length 92;
Best Local Similarity 27.2%; Pred. No. 0.0023;
Matches 22; Conservative 21; Mismatches 35; Indels

Db 62 DNDGBCDFQEFNFVAVMT 82

RESULT 12
US-07-987-272A-9
; Sequence 9, Application US/07987272A
; Patent No. 5731166
; GENERAL INFORMATION:
; APPLICANT: Geczy, C., Simpson, R. J. and Lackmann, M
; TITLE OF INVENTION: No. 5731166e1 Chemotactic Factor
; NUMBER OF SEQUENCES: 23

ADDRESSEE: Cushman Darby & Cushman
STREET: 1100 New York Avenue, N. W., Ninth Floor
CITY: Washington
STATE: D. C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/987,272A
FILING DATE: 05-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK 2127
FILING DATE: 05-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK 4463
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Brinkman, David W
REGISTRATION NUMBER: 20,817
REFERENCE/DOCKET NUMBER: DWB/1925/200259
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861 3000
TELEFAX: 202-822 0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-07-987-272A-9

Query Match 13.0%; Score 96; DB 1; Length 95;
Best Local Similarity 26.6%; Pred. No. 0.0045;
Matches 21; Conservative 18; Mismatches 40; Indels 0; Gaps 0;

QY 54 SLEKAIATATLIFRNSSDGKLEKAIKADLLQTFRNFAGQETKPKYREILSELDEH 113
DB 2 SOVEHAMEMTTFKFKACKGYLKEDLRLVMEKFEFGFLENQKDPDPLANDKIMKDLQOC 61

QY 114 TENKLDFFEDFMILLISITV 132
DB 62 RDCKVGQSFSSLIAGLTI 80

RESULT 13

US-08-918-727-7
; Sequence 7, Application US/08918727
; Patent No. 5849528
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Corley, Neil C.
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN S100 PROTEINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/918,727
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0373 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 488157

US-08-918-727-7

Query Match 13.0%; Score 96; DB 2; Length 113;
Best Local Similarity 30.1%; Pred. No. 0.0056;
Matches 25; Conservative 20; Mismatches 34; Indels 4; Gaps 2;

QY 49 ALRKCSDEKAIATATLIFRNSSDG---KLEKAIKADLLQTFRNFAGQETKPK-YR 104
DB 2 AAKTGSQERSISTINVFHQYSRKYGHPTLNKAEFKEMVKNKDLNFKREKRNENLLR 61

QY 105 EILSELDEHTENKLDFFEDFMILL 127
DB 62 DIMEDLTNQDNQLSFECNMMLM 84

RESULT 14

US-09-205-680A-7
; Sequence 7, Application US/09205680A
; Patent No. 6103497
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Corley, Neil C.
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN S100 PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/205,680A
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Colette C. Muenzen
REGISTRATION NUMBER: 39,784
REFERENCE/DOCKET NUMBER: PF-0373 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 486157

US-09-205-680A-7

Query Match 13.0%; Score 96; DB 3; Length 113;
Best Local Similarity 30.1%; Pred. No. 0.0058;
Matches 25; Conservative 20; Mismatches 34; Indels 4; Gaps 2;

QY 49 ALRKCSDEKAIATATLIFRNSSDG---KLEKAIKADLLQTFRNFAGQETKPK-YR 104
DB 2 AAKTGSQERSISTINVFHQYSRKYGHPTLNKAEFKEMVKNKDLNFKREKRNENLLR 61

QY 105 EILSELDEHTENKLDFFEDFMILL 127
DB 62 DIMEDLTNQDNQLSFECNMMLM 84

RESULT 15

US-07-987-272A-1
; Sequence 1, Application US/07987272A
; Patent No. 5731166
; GENERAL INFORMATION:

APPLICANT: Geczy, C., Simpson, R. J. and Lackmann, M
TITLE OF INVENTION: No. 5731166el Chemotactic Factor
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cushman Darby & Cushman
STREET: 1100 New York Avenue, N. W., Ninth Floor, East Tower
CITY: Washington
STATE: D. C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/987,272A
FILING DATE: 05-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK 2127
FILING DATE: 05-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK 4463
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Brinkman, David W
REGISTRATION NUMBER: 20,817
REFERENCE/DOCKET NUMBER: DWB/1925/200259
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861 3000
TELEFAX: 202-822 0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-987-272A-1

Query Match 12.3%; Score 91.5; DB 1; Length 88;
Best Local Similarity 27.4%; Pred. No. 0.013;
Matches 23; Conservative 23; Mismatches 31; Indels 7; Gaps 2;
QY 54 SDLEKAIATATLIFRNSSDSGK--LEKATAKLLQTPRNFAGQETPKYREILSEL 110
DB 2 SELEKALNLDIVHNSYNIQNHLYNDFKKAVTTECPQVQNINENLFR----EL 57
QY 111 DEHTENKLDFFDFMILLSITVMS 134
DB 58 DINSNDNAINFEFLAWIKVGVAS 81

Search completed: June 3, 2004, 13:23:02
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2004, 13:14:01 ; Search time 56 Seconds
(without alignments)
741.687 Million cell updates/sec

Title: US-09-744-197-1
Perfect score: 741
Sequence: 1 MG3CMHSTQKSLHLEDPN.....LSITVMSDLLQNRNWKIMK 147

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	741	100.0	147	3	AY58793 Human cal
2	715	96.5	143	4	AA40026 Human pol
3	690	93.1	140	4	AAU16494 Human nov
4	690	93.1	140	6	ABU55563 Human nov
5	686	92.6	137	4	AA41812 Human pol
6	138.5	18.7	93	7	ABE61762 Rat Prote
7	131.5	17.7	93	7	ABE61764 Human Pro
8	131.5	17.7	94	3	AA45531 Human S10
9	131.5	17.7	94	4	AA40258 Human pol
10	131.5	17.7	94	5	ABG96406 Human ova
11	123	16.6	97	2	AA27058 Sequence
12	123	16.6	97	2	AA26406 Sequence
13	123	16.6	97	3	AA45532 Human S10
14	123	16.6	97	5	ABG96408 Human ova
15	123	16.6	97	6	ABR92148 Human cer
16	123	16.6	97	7	ABD70348 Human cal
17	123	16.6	97	7	ABD59560 Human Pro
18	123	16.6	97	7	ABD59556 Human Pro
19	123	16.6	98	6	ABP71986 Human sta
20	123	16.6	98	6	ABU56414 Lung canc
21	123	16.6	98	6	ABU56415 Lung canc
22	123	16.6	98	6	ABU56412 Lung canc
23	111.5	15.0	124	6	ABU56412 Lung canc
24	108.5	14.6	134	6	ABR48453 Human S-1
25	106.5	14.4	101	2	AA20560 Human mts

26	106.5	14.4	101	2	AA20560 Human mts
27	106.5	14.4	101	3	AA45534 Human S10
28	106.5	14.4	101	3	AA37432 Human mts
29	106.5	14.4	101	4	AA37432 Human mts
30	106.5	14.4	101	6	ABU08513 Human mts
31	106.5	14.4	101	7	ABU08513 Human mts
32	106.5	14.4	134	3	ABU08513 Human mts
33	103	13.9	186	5	ABP42972 Human ova
34	102.5	13.8	97	5	ABP42972 Human ova
35	102.5	13.8	97	6	ABU11560 Human MDD
36	102.5	13.8	101	4	ABU11560 Human MDD
37	100	13.5	118	5	ABP42157 Human ova
38	98.5	13.3	92	5	ABP42157 Human ova
39	98.5	13.3	92	6	ABR58703 Human can
40	98.5	13.3	92	6	ABR58703 Human can
41	98.5	13.3	92	7	ABU63333 Human S10
42	98.5	13.3	92	8	ABU63333 Human S10
43	98.5	13.3	153	7	ABU63333 Human S10
44	98	13.2	152	4	AA39994 Human pol
45	96.5	13.0	91	2	AA46607 Human bra

ALIGNMENTS

RESULT 1

AY58793
ID AY58793 standard; protein; 147 AA.

XX AC AY58793;

DT DT 08-MAY-2000 (first entry)

XX DE Human calcium regulatory protein CaREG-1.

XX KW Human; calcium regulatory protein 1; CaREG-1; anticonvulsant; vasotropic;
cerebroprotective; neurotropic; neuroprotective; neuroleptic; cardiant;
cytostatic; epilepsy; stroke; Alzheimer's disease; cardiomyopathy;
KW myocarditis; Duchenne's muscular dystrophy; tachyarrhythmia; cancer;
diagnosis; therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Region 1..98 /note= "similarity to annexin type I signature"

FT Modified-site 7 /note= "potential O-phosphorylation"

FT Modified-site 39 /note= "potential O-phosphorylation"

FT Modified-site 54 /note= "potential O-phosphorylation"

FT Region 60..144 /note= "similarity to S100 Ca2+ binding protein signature"

FT Domain 60..144 /note= "similarity to EF-hand calcium binding domain"

FT Modified-site 69 /note= "potential N-glycosylation"

FT Modified-site 71 /note= "potential O-phosphorylation"

FT Modified-site 108 /note= "potential O-phosphorylation"

FT Region 115..128 /note= "similarity to annexin type I signature"

XX WO200005368-A1.

XX PD 03-FEB-2000.

XX EF 19-JUL-1999; 99WO-US012385.

XX PR 20-JUL-1998; 98US-0160076P.

XX PA (INCY-) INCYTE PHARM INC.
XX PI Bandman O, Tang YT, Corley NC, Guegler KJ, Baughn MR, Junming Y;
XX PI MPI; 2000-182695/16.
XX DR N-PSDB; AAZ58233.
XX PT New regulatory proteins and polynucleotides useful for treating and
XX PT detecting neurological disorders including epilepsy, Alzheimer's disease,
XX PT and stroke and cardiovascular disorders e.g. cardiomyopathy, myocarditis,
XX PT tachyarrhythmia.
XX PS Claim 1; Fig 1A-B; 74pp; English.
XX CC The present sequence is that of novel human calcium regulatory protein 1
XX CC (CAREG-1), as deduced from a consensus sequence (see AAZ58233) of
XX CC isolated cDNA clones. The protein has chemical and structural similarity
XX CC with human S100-alpha. Northern analysis showed that CAREG-1 is expressed
XX CC exclusively in lung tissue, including foetal and cancerous lung tissue.
XX CC The invention provides CAREG-1 and CAREG-2 polynucleotides and
XX CC polypeptides, expression vectors, host cells, antibodies, agonists and
XX CC antagonists. The polypeptides, polynucleotides and agonists are useful
XX CC for treating or preventing neurological disorders such as epilepsy, and
XX CC ischaemic cerebrovascular diseases, stroke, Alzheimer's disease etc., and
XX CC cardiovascular disorders such as cardiomyopathy, myocarditis, Duchenne's
XX CC muscular dystrophy, tachyarrhythmia etc. Antagonists and vectors
XX CC comprising antisense sequences are useful for treating and preventing
XX CC cancers such as adenocarcinoma, leukaemia, lymphoma and melanoma
XX SQ Sequence 147 AA;

Query Match 100.0%; Score 741; DB 3; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.6e-68;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGGCWHSTQDKSLHLEGDNPSPAPTSTCAPRMPKRIISIKOLASVKALRCSLEKAI 60
Db 1 MGGCWHSTQDKSLHLEGDNPSPAPTSTCAPRMPKRIISIKOLASVKALRCSLEKAI 60
Qy 61 ATTALIFRNSSDSGKLEKAIADKLLQTPRNPFAEQETPKPKYREILSELDEHTENKLD 120
Db 61 ATTALIFRNSSDSGKLEKAIADKLLQTPRNPFAEQETPKPKYREILSELDEHTENKLD 120
Qy 121 EDFMILLSTVMSDLLQNRNVKIMK 147
Db 121 EDFMILLSTVMSDLLQNRNVKIMK 147

RESULT 2
AAW40026
ID AAW40026 standard; protein; 143 AA.
XX AC AAW40026;
XX DT 22-OCT-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 3171.
XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX KW peripheral nervous system; neuropathy; central nervous system; CNS;
XX KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX KW leukaemia.
XX OS Homo sapiens.
XX PN WO20015312-A1.
XX PD 26-JUL-2001.
XX PF 26-DEC-2000; 2000WO-US034263.

XX PR 23-DEC-1999; 99US-00471275.
XX PR 21-JAN-2000; 2000US-00488725.
XX PR 25-APR-2000; 2000US-00552317.
XX PR 20-JUN-2000; 2000US-0058042.
XX PR 19-JUL-2000; 2000US-00620312.
XX PR 03-AUG-2000; 2000US-00653450.
XX PR 14-SEP-2000; 2000US-00662191.
XX PR 19-OCT-2000; 2000US-00693036.
XX PR 29-NOV-2000; 2000US-00727344.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
XX PI Zhou P, Goodrich R, Drmanac RT;
XX WPI; 2001-442253/47.
XX DR N-PSDB; AA159182.
XX PT Novel nucleic acids and polypeptides, useful for treating disorders such
XX PT as central nervous system injuries.
XX PS Example 4; SEQ ID NO 3171; 10078pp; English.
XX CC The invention relates to human nucleic acids (AA157798-AA161369) and the
XX CC encoded polypeptides (AA138642-AA142213) with nootropic,
XX CC immunosuppressant and cytostatic activity. The polynucleotides are useful
XX CC in gene therapy. A composition containing a polypeptide or polynucleotide
XX CC of the invention may be used to treat diseases of the peripheral nervous
XX CC system, such as peripheral nervous injuries, peripheral neuropathy and
XX CC localised neuropathies and central nervous system diseases, such as
XX CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX CC utilisation of the activities such as: Immune system suppression,
XX CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX CC assays for receptor activity, arthritis and inflammation, leukaemias and
XX CC C.N.S disorders. Note: The sequence data for this patent did not form
XX CC part of the printed specification
XX SQ Sequence 143 AA;

Query Match 96.5%; Score 715; DB 4; Length 143;
Best Local Similarity 100.0%; Pred. No. 3e-65;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 MHSTQDKSLHLEGDNPSPAPTSTCAPRMPKRIISIKOLASVKALRCSLEKAIATTA 64
Db 1 MHSTQDKSLHLEGDNPSPAPTSTCAPRMPKRIISIKOLASVKALRCSLEKAIATTA 60
Qy 65 LIFRNSSDSGKLEKAIADKLLQTPRNPFAEQETPKPKYREILSELDEHTENKLD 124
Db 61 LIFRNSSDSGKLEKAIADKLLQTPRNPFAEQETPKPKYREILSELDEHTENKLD 120
Qy 125 ILLLSITVMSDLLQNRNVKIMK 147
Db 121 ILLLSITVMSDLLQNRNVKIMK 143

RESULT 3
AAU16494
ID AAU16494 standard; protein; 140 AA.
XX AC AAU16494;
XX DT 07-NOV-2001 (first entry)
XX DE Human novel secreted protein, Seq ID 1447.
XX KW Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
XX KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
XX KW antibacterial; virucide; fungicide; ophthalmological; vulnerary;

KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KW cerebral ischaemia; angiogenesis; nervous system disorder;
KW Alzheimer's disease; infection; ocular disorder; corneal infection;
KW wound healing; epithelial cell proliferation; skin ageing; food additive;
KW preservative; antiproliferative.
XX Homo sapiens.
XX WO200155322-A2.
PD 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US001341.
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 02-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-020515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218230P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234232P.
PR 21-SEP-2000; 2000US-0234233P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 03-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.

PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-488783/53.
XX N-PSDB; AAS26481.
DR
XX New nucleic acid molecules encoding 461 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
PS Claim 11; SEQ ID NO 1447; 980pp; English.
XX
CC The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Antibodies to the proteins can also be used in
CC alleviating symptoms associated with the disorders and in diagnostic
CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays
CC (ELISA). Disorders which are diagnosed or treated include autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,
CC nervous system disorders e.g. Alzheimer's disease, infections caused by
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
CC and many other disorders listed in the specification. The polypeptides
CC can also be used to aid wound healing and epithelial cell proliferation,
CC to prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present
CC sequence represents a novel secreted protein of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC
Query Match 93.1%; Score 690; DB 4; Length 140;
Best Local Similarity 99.3%; Pred. No. 1.1e-62;
Matches 138; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 9 QDKSLHLEGDNPNSAAPTGTCAPRKMPKRIISIKQLASVKALKRKCSDLEKAIATTALIFR 68
Db :|||||
2 EDKSLHLEGDNPNSAAPTGTCAPRKMPKRIISIKQLASVKALKRKCSDLEKAIATTALIFR 61
QY 69 NSSDSGKLEKAIKALLOLQTFNFAEGQETPKYREILSELDEHTENKLDPEDFMILL 128
Db :|||||
62 NSSDSGKLEKAIKALLOLQTFNFAEGQETPKYREILSELDEHTENKLDPEDFMILL 121
QY 129 SITVMSDLLQNIIRNVKIMK 147
Db 122 SITVMSDLLQNIIRNVKIMK 140
RESULT 4
ABU55563
ID ABU555563 standard; protein; 140 AA.
AC ABU55563;
XX
XX 18-MAR-2003 (first entry)
DT
XX
DE Human novel polypeptide #650.
XX
XX Human; neural disorder; immune system disorder; renal disorder;
KW muscular disorder; respiratory disease; reproductive disorder;
XX

KW gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;
KW hyperproliferative disorder; inflammatory disease; allergic reaction;
KW blood related disorder; cancer; immunosuppressive; antiinflammatory;
KW cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;
KW haemostatic; antiarteriosclerotic.
XX
OS Homo sapiens.
XX
XX US2002132753-A1.
XX
XX 19-SEP-2002.
PD
XX
XX 17-JAN-2001; 2001US-00764864.
PF
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 22-AUG-2000; 2000US-0226868P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 08-SEP-2000; 2000US-0231413P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-024185P.
PR 01-NOV-2000; 2000US-0244617P.
PR 17-NOV-2000; 2000US-0249299P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
XX
XX (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
XX Rosen CA, Ruben SM, Barash SC;
PI
XX WPI; 2003-147444/14.
DR N-PSDB; ABX73822.
XX

XX New polypeptides and nucleic acids, useful in gene therapy for treating,
 PT inhibiting or preventing e.g. neural, immune system, muscular,
 PT respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
 PT renal disorders.

PS Claim 11; SEQ ID NO 1447; 402pp; English.

XX The invention relates to human novel polypeptides and their associated
 CC polynucleotides. The polypeptides and polynucleotides are useful in gene
 CC therapy for treating, inhibiting or preventing neural disorders, immune
 CC system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis
 CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g.
 CC nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders,
 CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
 CC (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left
 CC heart syndrome), renal disorders (e.g. acute kidney failure and end-stage
 CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and
 CC leukaemia), inflammatory diseases (e.g. septic shock, bursitis and
 CC appendicitis), allergic reactions and conditions (e.g. asthma), blood
 CC related disorders (e.g. thrombosis, atherosclerosis and myocardial
 CC infarction) and cancerous diseases. Sequences ABUS54914-ABUS5699 and
 CC ABUS5748 represent human novel polypeptides of the invention

XX Sequence 140 AA;

Query Match 93.1%; Score 690; DB 6; Length 140;

Best Local Similarity 99.3%; Pred. No. 1.1e-62;

Matches 138; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 QDKSLHLEGGDPNPSAAPTSCAPRKMPKRISISKQLASVKALKKCSLDLEKAIATTA 68

Db 2 EDKSLHLEGGDPNPSAAPTSCAPRKMPKRISISKQLASVKALKKCSLDLEKAIATTA 61

QY 69 NSSDSGKLEKAIADLLQTFRNFAEGQETPKYREILSELDEHTENKLDPEDFMILL 128

Db 62 NSSDSGKLEKAIADLLQTFRNFAEGQETPKYREILSELDEHTENKLDPEDFMILL 121

QY 129 SITVMSDLLQNRVKNK 147

Db 122 SITVMSDLLQNRVKNK 140

RESULT 5

AA41812

ID AA41812 standard; protein; 137 AA.

AC AA41812;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 6743.

KW Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

OS Homo sapiens.

XX WO200153312-A1.

PN 26-JUL-2001.

PD 26-DEC-2000; 2000WO-US034263.

PF 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-00552317.

PR 20-JUN-2000; 2000US-00598042.

PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;

DR WPI; 2001-442253/47.
 DR N-FSDS; AAI60968.

XX Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.

XX Example 2; SEQ ID NO 6743; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 CC encoded polypeptides (AAI38642-AAI42213) with nontropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as; Immune system suppression,
 CC Activin/inhibin activity, chemocactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification

XX Sequence 137 AA;

Query Match 92.8%; Score 686; DB 4; Length 137;

Best Local Similarity 100.0%; Pred. No. 2.7e-62;

Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 MHSTQDKSLHLEGGDPNPSAAPTSCAPRKMPKRISISKQLASVKALKKCSLDLEKAIATTA 64

Db 1 MHSTQDKSLHLEGGDPNPSAAPTSCAPRKMPKRISISKQLASVKALKKCSLDLEKAIATTA 60

QY 65 LIFRNSDSGKLEKAIADLLQTFRNFAEGQETPKYREILSELDEHTENKLDPEDFM 124

Db 61 LIFRNSDSGKLEKAIADLLQTFRNFAEGQETPKYREILSELDEHTENKLDPEDFM 120

QY 125 ILLLSITVMSDLLQNR 141

Db 121 ILLLSITVMSDLLQNR 137

RESULT 6

ADE61762

ID ADE61762 standard; protein; 93 AA.

XX ADE61762;

XX 29-JAN-2004 (first entry)

DE Rat Protein AAB20539, SEQ ID NO 7689.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

OS Rattus norvegicus.

XX WO2003016475-A2.

PN 27-FEB-2003.

PD 27-FEB-2003.

spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
Homo sapiens.
WO2003016475-A2.
27-FEB-2003.
14-AUG-2002; 2002WO-US025765.
14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
(GCHO) GEN HOSPITAL CORP.
(FARB) BAYER AG.
Woolf C, D'urso D, Befort K, Costigan M;
WPI; 2003-268312/26.
GENBANK; P23297.
New composition comprising two or more isolated polypeptides, useful for
preparing a medicament for treating pain in an animal.
Claim 1; Page; 1017pp; English.
The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
derivative or allelic variation of the nucleic acid sequence. Also
claimed are a vector comprising the novel polynucleotide, a host cell
comprising the vector, a method for identifying a nucleotide sequence
which is differentially regulated in an animal subjected to pain and a
kit to perform the method, an array, a method for identifying an agent
that increases or decreases the expression of the polynucleotide sequence
that is differentially expressed in neuronal tissue of a first animal
subjected to pain, a method for identifying a compound which regulates
the expression of a polynucleotide sequence which is differentially
expressed in an animal subjected to pain, a method for identifying a
compound that regulates the activity of one or more of the
polynucleotides, a method for producing a pharmaceutical composition, a
method for identifying a compound or small molecule that regulates the
activity in an animal of one or more of the polypeptides given in the
specification, a method for identifying a compound useful in treating
pain and a pharmaceutical composition comprising the one or more
polypeptides or their antibodies. The polynucleotide or the compound that
modulates its activity is useful for preparing a medicament for treating
pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
therapy). The sequence presented is a human protein (shown in Table 2 of
the specification) which is differentially expressed during pain. Note:
The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic form directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

14-AUG-2002; 2002WO-US025765.
14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
(GCHO) GEN HOSPITAL CORP.
(FARB) BAYER AG.
Woolf C, D'urso D, Befort K, Costigan M;
WPI; 2003-268312/26.
GENBANK; AAB20539.
New composition comprising two or more isolated polypeptides, useful for
preparing a medicament for treating pain in an animal.
Claim 1; Page; 1017pp; English.
The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
derivative or allelic variation of the nucleic acid sequence. Also
claimed are a vector comprising the novel polynucleotide, a host cell
comprising the vector, a method for identifying a nucleotide sequence
which is differentially regulated in an animal subjected to pain and a
kit to perform the method, an array, a method for identifying an agent
that increases or decreases the expression of the polynucleotide sequence
that is differentially expressed in neuronal tissue of a first animal
subjected to pain, a method for identifying a compound which regulates
the expression of a polynucleotide sequence which is differentially
expressed in an animal subjected to pain, a method for identifying a
compound that regulates the activity of one or more of the
polynucleotides, a method for producing a pharmaceutical composition, a
method for identifying a compound or small molecule that regulates the
activity in an animal of one or more of the polypeptides given in the
specification, a method for identifying a compound useful in treating
pain and a pharmaceutical composition comprising the one or more
polypeptides or their antibodies. The polynucleotide or the compound that
modulates its activity is useful for preparing a medicament for treating
pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
therapy). The sequence presented is a rat protein (shown in Table 2 of
the specification) which is differentially expressed during pain. Note:
The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic form directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

18.7%; Score 138.5; DB 7; Length 93;
Query Match
Best Local Similarity 36.6%; Pred. No. 2.5e-06;
Matches 30; Conservative 21; Mismatches 28; Indels 3; Gaps 1;
Sequence 93 AA;
54 SDLEKAIATTAIFRNSSDSG---KLEKAIADLLQTFRNFAGQETPKYREILSEL 110
2 SELETAMETLINVFHAGSGEGDKYKLSKKEKLLQTELSSFLDVQKADAVDKIMKEL 61
111 DEHTENKLDPEDFMILLSTIV 132
DENGGEVDVFQEFVVLVAALTV 83
ADBE61764 standard; protein; 93 AA.
ADBE61764;
29-JAN-2004 (first entry)
Human Protein P23297, SEQ ID NO 7691.
Human; pain; neuronal tissue; gene therapy;

17.7%; Score 131.5; DB 7; Length 93;
Query Match
Best Local Similarity 32.9%; Pred. No. 1.3e-05;
Matches 27; Conservative 23; Mismatches 29; Indels 3; Gaps 1;
Sequence 93 AA;
54 SDLEKAIATTAIFRNSSDSG---KLEKAIADLLQTFRNFAGQETPKYREILSEL 110
2 SELETAMETLINVFHAGSGEGDKYKLSKKEKLLQTELSSFLDVQKADAVDKIMKEL 61
111 DEHTENKLDPEDFMILLSTIV 132
DENGGEVDVFQEFVVLVAALTV 83
RESULT 8
AAB45531

ID AAB45531 standard; protein; 94 AA.

XX AC AAB45531;

XX DT 22-FEB-2001 (first entry)

XX DE Human S100A1 protein.

XX KW S100 protein; human; treatment; cardiomyopathy; cardiac insufficiency;
KW calcium-binding protein; calcium homeostasis; cardiac muscle;
KW pumping capacity; myocardial cell; systolic calcium ion release;
KW sarcoplasmic reticulum; cardiac disease; hypertension; rhythm disorder;
KW valve defect.

XX OS Homo sapiens.

XX PN DE19915485-A1.

XX PD 19-OCT-2000.

XX PF 07-APR-1999; 99DE-01015485.

XX PR 07-APR-1999; 99DE-01015485.

XX PA (KATU/) KATUS H A.
PA (REMP/) REMPPIS A.

XX PI Katus HA, Remppis A;

XX PR WPI; 2000-673510/66.

XX DR N-PSDB; AAC81801.

XX PT Composition containing S100 protein, corresponding nucleic acid or
PT vector, useful for treating cardiomyopathy and cardiac insufficiency.

XX PS Claim 10; Page 8; 36pp; German.

XX This invention describes a novel composition for treating primary or
CC secondary cardiomyopathy or cardiac insufficiency contains at least one
CC S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or
CC fragments, or a gene transfer vector containing (II), optionally
CC formulated with auxiliaries and/or carriers. (I) are calcium-binding
CC proteins involved in calcium homeostasis, so their overexpression in
CC cardiac muscle will improve pumping capacity (and overall capacity) of
CC the heart. In cultured myocardial cells they increase the contraction and
CC relaxation rates associated with increased systolic calcium ion release
CC from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are
CC used to treat cardiomyopathy (CMP) where inherited or caused by
CC spontaneous mutations and ischemic CMP caused by arteriosclerosis,
CC dilative CMP caused by toxic/infectious disease, cardiac disease caused
CC by pulmonary and/or arterial hypertension, and structural disease caused
CC by rhythm disorders or valve defects, generally any condition associated
CC with reduced contractile force. Unlike calmodulin, which is expressed
CC ubiquitously, (I) show tissue-specific expression and treat the
CC underlying defect in the sarcoplasmic reticulum (SR) that causes cardiac
CC disease

XX SQ Sequence 94 AA;

Query Match 17.7%; Score 131.5; DB 3; Length 94;

Best Local Similarity 32.9%; Pred. No. 1.3e-05;

Matches 27; Conservative 23; Mismatches 29; Indels 3; Gaps 1;

QY 54 SDLEKAIATTAIFRNSDSG---KLEKAKADLLQTOFRNFAEQGTPKPKYREILSEL 110

DB 3 SELETAMETLINVFHAHSGEGDKYKLSKKELKELLQTELSGFLDAQKDVAQDKVMKEL 62

QY 111 DEHTENKLDFFEDFMILLISITV 132

DB 63 DENGSGEVDFOBYVVLVAALTV 84

RESULT 9

AAM40258

ID AAM40258 standard; protein; 94 AA.

XX AC AAM40258;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 3403.

XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX OS Homo sapiens.

XX PN WO200153312-A1.

XX PD 26-JUL-2001.

XX PF 26-DEC-2000; 2000WO-US034263.

XX PR 23-DEC-1999; 99US-00471275.

XX PR 21-JAN-2000; 2000US-00488725.

XX PR 25-APR-2000; 2000US-00552317.

XX PR 20-JUN-2000; 2000US-00598042.

XX PR 19-JUL-2000; 2000US-00620312.

XX PR 03-AUG-2000; 2000US-00653450.

XX PR 14-SEP-2000; 2000US-00682191.

XX PR 19-OCT-2000; 2000US-00695036.

XX PR 29-NOV-2000; 2000US-00727344.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;

XX PI Zhou P, Goodrich R, Drmanac RT;

XX DR WPI; 2001-442253/47.

XX DR N-PSDB; AAI59414.

XX PT Novel nucleic acids and polypeptides, useful for treating disorders such
XX as central nervous system injuries.

XX PS Example 5; SEQ ID NO 3403; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX SQ Sequence 94 AA;

Query Match 17.7%; Score 131.5; DB 4; Length 94;

Best Local Similarity 32.9%; Pred. No. 1.3e-05;

Matches 27; Conservative 23; Mismatches 29; Indels 3; Gaps 1;

QY 54 SDLEKAIATTAIFRNSDSG---KLEKAIKADLLQTOFRNFAEQGTPKPKYREILSEL 110

DB 3 SELETAMETLINVFHAHSGEGDKYKLSKKELKELLQTELSGFLDAQKDVAQDKVMKEL 62

CC disease or atherosclerosis). The compositions and methods may also be
 CC used in assessing the histological type of neoplasm associated with
 CC ovarian cancer, monitoring the progression of ovarian cancer, determining
 CC whether ovarian cancer has metastasized or is likely to metastasize,
 CC selecting a composition for inhibiting ovarian cancer, assessing the
 CC ovarian carcinogenic potential of a compound, or inhibiting ovarian
 CC cancer or at risk of developing ovarian cancer. The present amino acid
 CC sequence represents one of the ovarian cancer markers described in the
 CC invention

XX SQ Sequence 94 AA;

Query Match 17.7%; Score 131.5; DB 5; Length 94;
 Best Local Similarity 32.9%; Pred. No. 1.3e-05;
 Matches 27; Conservative 23; Mismatches 29; Indels 3; Gaps 1;

Qy 54 SDEKAIATATLAFRNSSDG---KLEKAIADLLQTFRNPAGQETPKYKREILSEL 110
 Db 3 SELETAMETINVFHAHSGKGGKYLKSKKELKQLTELQSLGFLDAQKQVDAYDKVMKEL 62

Qy 111 DEHTENKLPDEFMILLISITY 132
 Db 63 DENGGEVDFQEVVLVAALTIV 84

RESULT 11
 AAR27058
 ID AAR27058 standard; protein; 97 AA.
 XX
 AC AAR27058;
 XX
 DT 25-MAR-2003 (revised)
 DT 25-FEB-1993 (first entry)
 XX
 DE Sequence of small Ca++ binding proteins encoded by Can19 clone 19.
 XX
 KW Can19; tumour suppressor gene; cancer; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9215602-A1.
 XX
 PD 17-SEP-1992.
 XX
 PF 28-FEB-1992; 92WO-US001624.
 XX
 PR 28-FEB-1991; 91US-00662216.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 XX
 PI Sager R;
 XX
 DR WPI; 1992-331663/40.
 DR N-PSDB; AAQ28760.
 XX
 PT Diagnosis and treatment of cancer - using candidate tumour suppressor
 PT genes or the corresp. antibodies.
 XX
 PS Disclosure; Page 31; 54pp; English.
 XX

CC A clone originally termed clone 19, and now referred to as Can19,
 CC represents a gene expressed in normal mammary epithelial cell strains but
 CC not in tumor-derived cell lines. Sequence comparisons have shown that
 CC Can19 is a member of the S100 gene family, encoding small Ca++ binding
 CC proteins (about 10 kD) with diverse functions. These proteins have two
 CC "EF hands", domains where Ca2+ is bound. Can19 is also related in
 CC structure to the small regulatory subunit of calpactin, p11. Can19 is not
 CC expressed in breast tumor cells. Can19 appears to be negatively regulated
 CC in tumors, in contrast to calycclin. (Updated on 25-MAR-2003 to correct
 CC PN field.) (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 97 AA;

Qy 111 DEHTENKLPDEFMILLISITY 132
 Db 63 DENGGEVDFQEVVLVAALTIV 84

RESULT 10
 ABG96406
 ID ABG96406 standard; protein; 94 AA.
 XX
 AC ABG96406;
 XX
 DT 11-DEC-2002 (first entry)
 DE Human ovarian cancer marker OV55.
 XX

XX Human; ovarian cancer; marker; cancer; familial history; brain disorder;
 KW central nervous system disorder; bacterial meningitis; viral meningitis;
 KW Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;
 KW brain herniation; inflammation; encephalitis; testicular disorder;
 KW nontuberculous granulomatous orchitis; connective tissue disorder;
 KW heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;
 KW histological type; carcinogenic; ovarian cancer marker.
 XX

OS Homo sapiens.
 XX
 PN WO200271928-A2.
 XX
 PD 19-SEP-2002.
 XX
 PF 14-MAR-2002; 2002WO-US007826.
 XX
 PR 14-MAR-2001; 2001US-0276025P.
 PR 14-MAR-2001; 2001US-0276026P.
 PR 10-AUG-2001; 2001US-0311732P.
 PR 19-SEP-2001; 2001US-0323580P.
 PR 26-SEP-2001; 2001US-0324967P.
 PR 26-SEP-2001; 2001US-0325102P.
 PR 26-SEP-2001; 2001US-0325149P.
 XX

(MILL-) MILLENNIUM PHARM INC.
 XX
 PI Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;
 PI Meyers RC, Morrisey MP, Olandt PO, Sen A, Vieby PO, Mills GB;
 PI East RE, Lu K, Schmandt RE, Zhao X, Glatt K;
 XX
 DR WPI; 2002-723277/78.
 DR N-PSDB; ABS76505.
 XX

PT Assessing whether a patient is afflicted with ovarian cancer, useful in
 PT assessing the stage or progression of the disease, comprises comparing
 PT the expression level of a cancer marker in a sample from a patient and
 PT from a non cancer patient.
 XX
 PS Disclosure; Page 391; 481pp; English.
 XX

CC The present invention relates to a new method for assessing whether a
 CC patient is afflicted with ovarian cancer. The method involves comparing
 CC the expression level of a marker in a patient sample and the normal level
 CC of expression of the marker in a control non-ovarian cancer sample, where
 CC the marker is selected from 363 cancer markers described in the
 CC specification. The method of the invention is useful in diagnosing or
 CC characterising cancer, in detecting the presence of cancer as early as
 CC possible, and the recurrence of ovarian cancer. The method may also be of
 CC particular use with patients having an enhanced risk of developing
 CC ovarian cancer (e.g. patients having a familial history of ovarian
 CC cancer). The cancer markers may be used in the management and treatment
 CC of e.g. brain and central nervous system disorders (e.g. bacterial and
 CC viral meningitis, Alzheimer's disease or Parkinson's disease), brain
 CC disorders (e.g. cerebral oedema, hydrocephalus or brain herniations),
 CC inflammations (e.g. bacterial or viral meningitis or encephalitis),
 CC testicular disorders (e.g. nontuberculous granulomatous orchitis),
 CC connective tissue disorders, or heart disorders (e.g. ischaemic heart

```
Query Match 16.6%; Score 123; DB 2; Length 97;
Best Local Similarity 31.1%; Pred. No. 0.0001;
Matches 28; Conservative 22; Mismatches 36; Indels 4; Gaps 2;

QY 53 CSDLEKATATTALIFRNSSDSG---KLEKAIADLLQTPRNFARQGTQPKYREILSE 109
DB 2 CSSLEQALAVLVTTFHKYSQCGDKFKLSRGEMKELLHKELPSFVGEKVDDEGLKLMGN 61

QY 110 LDEHTENKLDPEDFMILLISITVM-SDLLQ 138
DB 62 LDENSQQVDFOEYAVFLALITVMCNDFQ 91

RESULT 12
AAR26406
ID AAR26406 standard; protein; 97 AA.
XX
AC AAR26406;
XX
DT 25-MAR-2003 (revised)
DT 27-FEB-1993 (first entry)
XX
DE Sequence of the clone 19 gene product.
XX
KW Clone 19; diagnosis; prognosis; cancer; tumour.
XX
OS Homo sapiens.
XX
PN WO9215600-A1.
XX
PD 17-SEP-1992.
XX
PF 28-FEB-1992; 92WO-US001625.
XX
PR 28-FEB-1991; 91US-00662198.
XX
PA (DAND ) DANA FARBER CANCER INST INC.
XX
PI Sager R, Lee SW, Tomasetto C;
XX
WPI; 1992-331662/40.
DR N-PSDB; AAR26007.
XX
Clone 19 gene prodn. and its DNA and antibody - for diagnosis, prognosis
and treatment of solid tumours, especially breast cancer.
XX
PS Disclosure; Page 12-13; 20pp; English.
XX
Clone 19 was derived from normal human mammary epithelial cells strain
76N. Clone 19 represents a gene expressed in normal mammary epithelial
cell strains but not in tumour-derived cell lines. Sequence comparisons
have shown that it is a member of the S100 gene family, encoding small
Ca++ binding proteins (about 10kd) with diverse functions. These proteins
have two 'EF hands' domains where Ca++ is bound, in contrast to calmodulin
proteins which have four. Clone 19 is also related in structure to the
small regulatory subunit of calpactin, p11. MRP8 and MRP14 are also
related, and are S100 proteins expressed by macrophages during chronic
inflammation. (Updated on 25-MAR-2003 to correct PN field.) (Updated on
25-MAR-2003 to correct PA field.)
XX
Sequence 97 AA;

Query Match 16.6%; Score 123; DB 2; Length 97;
Best Local Similarity 31.1%; Pred. No. 0.0001;
Matches 28; Conservative 22; Mismatches 36; Indels 4; Gaps 2;

QY 53 CSDLEKATATTALIFRNSSDSG---KLEKAIADLLQTPRNFARQGTQPKYREILSE 109
DB 2 CSSLEQALAVLVTTFHKYSQCGDKFKLSRGEMKELLHKELPSFVGEKVDDEGLKLMGN 61

QY 110 LDEHTENKLDPEDFMILLISITVM-SDLLQ 138
DB 62 LDENSQQVDFOEYAVFLALITVMCNDFQ 91
```

RESULT 13

AAB45532
ID AAB45532 standard; protein; 97 AA.

XX
AC AAB45532;

XX
DT 22-FEB-2001 (first entry)

XX
DE Human S100A2 protein.

XX
KW S100 protein; human; treatment; cardiomyopathy; cardiac insufficiency;
calcium-binding protein; calcium homeostasis; cardiac muscle;
pumping capacity; myocardial cell; systolic calcium ion release;
sarcoplasmic reticulum; cardiac disease; hypertension; rhythm disorder;
valve defect.

XX
OS Homo sapiens.

XX
PN DE19915485-A1.

XX
PD 19-OCT-2000.

XX
PF 07-APR-1999; 99DE-01015485.

XX
PR 07-APR-1999; 99DE-01015485.

XX
PA (KATU/) KATUS H A.
PA (REMP/) REMPPIS A.

XX
PI Katus HA, Remppis A;

XX
DR WPI; 2000-673510/66.

XX
Composition containing S100 protein, corresponding nucleic acid or
vector, useful for treating cardiomyopathy and cardiac insufficiency.

XX
Claim 35; Page 9; 36pp; German.

XX
This invention describes a novel composition for treating primary or
secondary cardiomyopathy or cardiac insufficiency contains at least one
S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or
fragments, or a gene transfer vector containing (II), optionally
formulated with auxiliaries and/or carriers. (I) are calcium-binding
proteins involved in calcium homeostasis, so their overexpression in
cardiac muscle will improve pumping capacity (and overall capacity) of
the heart. In cultured myocardial cells they increase the contraction and
relaxation rates associated with increased systolic calcium ion release
from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are
used to treat cardiomyopathy (CMP) where inherited or caused by
spontaneous mutations and ischemic CMP caused by arteriosclerosis,
diabetic CMP caused by toxic/infectious disease, cardiac disease caused
by pulmonary and/or arterial hypertension, and structural disease caused
by rhythm disorders or valve defects, generally any condition associated
with reduced contractile force. Unlike calmodulin, which is expressed
ubiquitously, (I) show tissue-specific expression and treat the
underlying defect in the sarcoplasmic reticulum (SR) that causes cardiac
disease

XX
Sequence 97 AA;

Query Match 16.6%; Score 123; DB 3; Length 97;
Best Local Similarity 31.1%; Pred. No. 0.0001;
Matches 28; Conservative 22; Mismatches 36; Indels 4; Gaps 2;

QY 53 CSDLEKATATTALIFRNSSDSG---KLEKAIADLLQTPRNFARQGTQPKYREILSE 109
DB 2 CSSLEQALAVLVTTFHKYSQCGDKFKLSRGEMKELLHKELPSFVGEKVDDEGLKLMGS 61

QY 110 LDEHTENKLDPEDFMILLISITVM-SDLLQ 138

DB 62 LDENSQQVDFOEYAVFLALITVMCNDFQ 91

RESULT 14

ABG96408
ID ABG96408 standard; protein; 97 AA.

XX AC ABG96408;

XX DT 11-DEC-2002 (first entry)

XX DE Human ovarian cancer marker M68.

XX Human; ovarian cancer; marker; cancer; familial history; brain disorder;
XX central nervous system disorder; bacterial meningitis; viral meningitis;
XX Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;
XX brain herniation; inflammation; encephalitis; testicular disorder;
XX nontuberculous granulomatous orchitis; connective tissue disorder;
XX heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;
XX histological type; carcinogenic; ovarian cancer marker.

XX OS Homo sapiens.

XX PN WO200271928-A2.

XX PD 19-SEP-2002.

XX PF 14-MAR-2002; 2002WO-US007826.

XX PR 14-MAR-2001; 2001US-0276025P.

XX PR 14-MAR-2001; 2001US-0276026P.

XX PR 10-AUG-2001; 2001US-0311732P.

XX PR 19-SEP-2001; 2001US-0323580P.

XX PR 26-SEP-2001; 2001US-0324967P.

XX PR 26-SEP-2001; 2001US-0325102P.

XX PR 26-SEP-2001; 2001US-0325149P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;

XX PI Meyers RE, Morrissey MP, Olandt PJ, Sen A, Vieby PO, Mills GS;

XX PI Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;

XX WPI; 2002-723277/78.

XX DR N-PSDB; ABS76507.

XX Assessing whether a patient is afflicted with ovarian cancer, useful in
PT assessing the stage or progression of the disease, comprises comparing
PT the expression level of a cancer marker in a sample from a patient and
PT from a non cancer patient.

XX PS Disclosure; Page 392; 481pp; English.

XX The present invention relates to a new method for assessing whether a
CC patient is afflicted with ovarian cancer. The method involves comparing
CC the expression level of a marker in a patient sample and the normal level
CC of expression of the marker in a control non-ovarian cancer sample, where
CC the marker is selected from 363 cancer markers described in the
CC specification. The method of the invention is useful in diagnosing or
CC characterising cancer, in detecting the presence of cancer as early as
CC possible, and the recurrence of ovarian cancer. The method may also be of
CC particular use with patients having an enhanced risk of developing
CC ovarian cancer (e.g. patients having a familial history of ovarian
CC cancer). The cancer markers may be used in the management and treatment
CC of e.g. brain and central nervous system disorders (e.g. bacterial and
CC viral meningitis, Alzheimer's disease or Parkinson's disease), brain
CC disorders (e.g. cerebral oedema, hydrocephalus or brain herniations),
CC inflammations (e.g. bacterial or viral meningitis or encephalitis),
CC testicular disorders (e.g. nontuberculous granulomatous orchitis),
CC connective tissue disorders, or heart disorders (e.g. ischaemic heart
CC disease or atherosclerosis). The compositions and methods may also be
CC used in assessing the histological type of neoplasm associated with
CC ovarian cancer, monitoring the progression of ovarian cancer, determining
CC whether ovarian cancer has metastasized or is likely to metastasize,

CC selecting a composition for inhibiting ovarian cancer, assessing the
CC ovarian carcinogenic potential of a compound, or inhibiting ovarian
CC cancer or at risk of developing ovarian cancer. The present amino acid
CC sequence represents one of the ovarian cancer markers described in the
CC invention

XX SQ Sequence 97 AA;

Query Match 16.6%; Score 123; DB 5; Length 97;

Best Local Similarity 31.1%; Pred. No. 0.0001;

Matches 28; Conservative 22; Mismatches 36; Indels 4; Gaps 2;

QY 53 CSDLEKALATTALLFRNSSSDG--KLEKAIKDLLOTRNFAEQGQETPKKYRETLSE 109

DB 2 CSSLEQALAVLVITTFHKYSCQEGDKFKLSGEMKELLKELPSFVGKVDGGLKLMGS 61

QY 110 LDEHTENKLPEDFMILLLSITVM-SDLLQ 138

DB 62 LDNSDQQVDFQYAVFLALITVMCNDFQ 91

RESULT 15

ABR92148

ID ABR92148 standard; protein; 97 AA.

XX AC ABR92148;

XX DT 10-SEP-2003 (first entry)

XX DE Human cervical cancer cell marker protein SEQ ID NO:206.

XX Human; cervical cancer; cervical cancer marker; cancer therapy;

XX detection; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN WO2002101075-A2.

XX PD 19-DEC-2002.

XX PF 12-JUN-2002; 2002WO-US018638.

XX PR 13-JUN-2001; 2001US-0298155P.

XX PR 13-JUN-2001; 2001US-0298159P.

XX PR 14-NOV-2001; 2001US-0335936P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Schlegel R, Chen Y, Zhao X, Monahan JE, Kamatkar S;

XX PI Gannavarapu M, Glatt K, Hoersch S;

XX WPI; 2003-156967/15.

XX DR N-PSDB; ACF12931.

XX New isolated nucleic acid molecule useful for detecting, characterizing,
PT preventing and treating human cervical cancers, in various prognostic and
PT diagnostic assays, in pharmacogenomics and in monitoring clinical trials.

XX Claim 4; Page 361-362; 386pp; English.

XX ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I)
CC given in ABR92047 to ABR92164. A higher level of expression of (I) than
CC normal indicates the presence of cervical cancer. Also described: (1) a
CC vector (II) containing (I); (2) a host cell (III) containing (I); and (3)
CC assessing (M) whether a patient is afflicted with cervical cancer,
CC comprising comparing the level of expression of a marker in a patient's
CC sample, and the normal level of expression of the marker in a control non
CC cervical cancer sample, where a significant increase in the level of
CC expression of the marker in the patient's sample relative to that in the
CC control sample is an indication that the patient is afflicted with
CC cervical cancer. (I) has cytostatic activity, and can be used in gene
CC therapy and in vaccines. (I) is useful in detecting, characterising,
CC preventing and treating human cervical cancers. (I) may also be used in

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OM protein - protein search, using sw model

Run on: June 3, 2004, 13:26:27 ; Search time 40 Seconds
(without alignments)
1159.529 Million cell updates/sec

Title: US-09-744-197-1

Perfect score: 147

Sequence: 1 MGGCMHSTQDKSLHLEDPN.....LSITVMSDLLQNIERNVKIMK 147

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	12.2	147	11 Q8C9X1	Q8C9X1 mus musculus
2	9	6.1	360	10 Q940C2	Q940C2 arabidopsis
3	8	5.4	314	10 P93444	P93444 pyrolacc
4	8	5.4	424	11 Q99N63	Q99N63 mesocricetu
5	8	5.4	716	2 Q49526	Q49526 mycoplasma
6	8	5.4	730	10 Q9SKK7	Q9SKK7 arabidopsis
7	8	5.4	1051	2 Q49524	Q49524 mycoplasma
8	8	5.4	1344	2 Q49545	Q49545 mycoplasma
9	8	5.4	1365	2 Q49525	Q49525 mycoplasma
10	8	5.4	1860	5 Q9VYP5	Q9VYP5 drosophila
11	7	4.8	111	8 Q94RG1	Q94RG1 heterodoncu
12	7	4.8	111	16 Q8YKY3	Q8YKY3 anabaena sp
13	7	4.8	114	16 Q7URH0	Q7URH0 rhodospirell
14	7	4.8	116	8 Q94ZD6	Q94ZD6 eptatretus
15	7	4.8	130	16 Q7V175	Q7V175 prochloroco
16	7	4.8	131	11 Q8BYN5	Q8BYN5 mus musculu

17 7 4.8 145 4 Q9BXM9
18 7 4.8 156 16 Q8CS56
19 7 4.8 157 16 Q7UGD3
20 7 4.8 156 10 Q9ZRF2
21 7 4.8 172 13 Q13095
22 7 4.8 177 10 Q9FXT1
23 7 4.8 179 5 Q9VD02
24 7 4.8 185 16 Q67526
25 7 4.8 214 10 Q41899
26 7 4.8 220 17 Q974S7
27 7 4.8 234 1 Q72AH4
28 7 4.8 237 16 Q8UI09
29 7 4.8 247 10 Q40900
30 7 4.8 247 10 Q87111
31 7 4.8 259 10 Q24009
32 7 4.8 259 16 Q9K5U6
33 7 4.8 260 2 Q8GDY3
34 7 4.8 264 10 Q9ZS30
35 7 4.8 265 16 Q8DV40
36 7 4.8 269 10 Q8H281
37 7 4.8 273 10 Q84V80
38 7 4.8 277 2 Q8VUN3
39 7 4.8 291 17 Q8TPS8
40 7 4.8 295 16 Q9A2A7
41 7 4.8 295 16 Q894V2
42 7 4.8 304 10 Q84V75
43 7 4.8 309 16 Q89LT0
44 7 4.8 324 16 Q88Z06
45 7 4.8 341 8 Q8WE39

ALIGNMENTS

RESULT 1

Q8C9X1 PRELIMINARY; PRT; 147 AA.
ID Q8C9X1
AC Q8C9X1: 2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical EF-hand containing protein.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK040281; BAC30559.1; ..
DR GO; GO:0005509; F;calcium ion binding; IEA.
DR InterPro; IPR002048; EF-hand.
KW Hypothetical protein.
SQ SEQUENCE 147 AA; 16415 MW; FICE14DBFER26D59 CRC64;

Query Match 12.2%; Score 18; DB 11; Length 147;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 ILSELDHTENKLDPEDF 123
DB 106 ILSELDHTENKLDPEDF 123

RESULT 2

Q940C2 PRELIMINARY; PRT; 360 AA.
ID Q940C2

AC Q940C2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE AT952550/F6N7_3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RN Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L.,
RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis ORF clones.";
RN Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY056121; AAL07007.1; -;
DR EMBL; AY078034; AAL77735.1; -;
SQ SEQUENCE 360 AA; 41042 MW; E5991D998FF49F01 CRC64;

Query Match 6.1%; Score 9; DB 10; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 LEXA1ATTA 64
Db 143 LEXA1ATTA 151

RESULT 3
ID P93444 PRELIMINARY; PRT; 314 AA.
AC P93444;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pokeweed antiviral protein precursor (BC 3.2.2.22) (rRNA
DE N-glycosidase).
GN PAP-S.
OS Phytolacca americana (Common pokeberry) (Virginian pokeweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=3527;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Seed;
RX MEDLINE=97263479; PubMed=9109394;
RA Poyet J.L., Hoeveler A.;
RT "cDNA cloning of the gene encoding the Antiviral Protein from the
RT seeds of Phytolacca americana and its expression in E.coli.";
RL FEBS Lett. 406:97-100(1997)
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; X98079; CAA66702.1; -;

DR HSP; Q03464; IAPA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0017149; F:protein biosynthesis inhibitor activity; IEA.
DR GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR001574; RIF.
DR Pfam; PF00161; RIF; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA RICIN; 1.
KW Hydrolase; Signal; Toxin.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 314 POTENTIAL.
SQ SEQUENCE 314 AA; 35323 MW; A89B3CE57789FF9E CRC64;

Query Match 5.4%; Score 8; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AAPTSTCA 30
Db 17 AAPTSTCA 24

RESULT 4
ID Q99N63 PRELIMINARY; PRT; 424 AA.
AC Q99N63;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Homeobox B3.
GN HOX B3.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakamura N.;
RT "hamster Hox B3 cds.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AB056577; BAB33375.1; -;
DR HSP; P02833; 18AN.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00027; HOMEBOX; 1; 1.
DR PROSITE; PS00071; HOMEBOX; 2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 424 AA; 43631 MW; DC7E64040B8DA5A4 CRC64;

Query Match 5.4%; Score 8; DB 11; Length 424;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 PSAAPTST 28
Db 92 PSAAPTST 99

RESULT 5
Q49526

```
ID Q49526 PRELIMINARY; PRT; 716 AA.
AC Q49526;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Lmp1.
GN Lmp1.
OS Mycoplasma hominis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2098;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mh81;
RX MEDLINE=95369882; PubMed=7543881;
RA Jensen L.T., Ladefoged S., Birkelund S., Christiansen G.;
RT "Selection of Mycoplasma hominis PG21 deletion mutants by cultivation
in the presence of monoclonal antibody 552.";
RL Infect. Immun. 63:3336-3347(1995).
DR EMBL; U21963; AAA81014.1; -.
DR InterPro; IPR006864; LMP.
DR Pfam; PF04778; LMP; 4.
SQ SEQUENCE 716 AA; 79864 MW; 28D08C3E0C91CB47 CRC64;

Query Match 5.4%; Score 8; DB 2; Length 716;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 AIATTALI 66
DB 20 AIATTALI 27

RESULT 6
Q9SKK7 PRELIMINARY; PRT; 730 AA.
ID Q9SKK7;
AC Q9SKK7;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN AT2G25420.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
RA Fraser C.M., Venter J.C.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006300; AAD20702.2; -.
DR FIR; B84648; B84648.
DR InterPro; IPR006595; CTLH.
DR InterPro; IPR006594; LISH.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00668; CTLH; 2.
DR SMART; SM00667; LISH; 2.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS00897; CTLH; 1.
DR PROSITE; PS00896; LISH; 2.
DR PROSITE; PS00882; WD_REPEATS_2; 1.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Hypothetical protein_repeat; Repeat; WD repeat.
SQ SEQUENCE 730 AA; 82003 MW; 18205CE1D3769F88 CRC64;

Query Match 5.4%; Score 8; DB 10; Length 730;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 70 SSDSGKL 77
DB 541 SSDSGKL 548
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RESULT 7

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Q49524 PRELIMINARY; PRT; 1051 AA.
ID Q49524;
AC Q49524;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Lmp1.
GN Lmp1.
OS Mycoplasma hominis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2098;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mh74;
RX MEDLINE=95369882; PubMed=7543881;
RA Jensen L.T., Ladefoged S., Birkelund S., Christiansen G.;
RT "Selection of Mycoplasma hominis PG21 deletion mutants by cultivation
in the presence of monoclonal antibody 552.";
RL Infect. Immun. 63:3336-3347(1995).
DR EMBL; U21961; AAA81012.1; -.
DR FIR; T18351; T18351.
DR InterPro; IPR006864; LMP.
DR Pfam; PF04778; LMP; 2.
SQ SEQUENCE 1051 AA; 120260 MW; 82B311BB966BFF7E CRC64;
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Query Match 5.4%; Score 8; DB 2; Length 1051;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 59 AIATTALI 66
DB 20 AIATTALI 27
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RESULT 8

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Q49545 PRELIMINARY; PRT; 1344 AA.
ID Q49545;
AC Q49545;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Lmp1 protein.
GN Lmp1.
OS Mycoplasma hominis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2098;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PG21;
RX MEDLINE=95104998; PubMed=7806360;
RA Ladefoged S.A., Birkelund S., Rauge S., Brock B., Jensen L.T.,
RA Christiansen G.;
RT "A 135-kilodalton surface antigen of Mycoplasma hominis PG21 contains
multiple directly repeated sequences.";
RL Infect. Immun. 63:212-223(1995).
DR EMBL; X81475; CAA57228.1; -.
DR InterPro; IPR006864; LMP.
DR Pfam; PF04778; LMP; 8.
SQ SEQUENCE 1344 AA; 149405 MW; 6E0105F7365AF8CF CRC64;
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Query Match 5.4%; Score 8; DB 2; Length 1344;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 59 AIATTALI 66
DB 20 AIATTALI 27
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Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Holtin D., Houston K.A., Howland T.J., Wei M.-H., Ibgwan C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusser D.J., Pacle J.M.,
Palazzo R.M., Pittman G.S., Pan S., Pollard D.R., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Swirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of *Drosophila melanogaster*";
SEQUENCE 287:2195-2195(2000).
[2]
SEQUENCE FROM N.A.
RP CELINIKER S.E., ADAMS M.D., KRONMILLER B., WAN K.H., HOLT R.A.,
CELINIKER S.E., COCAYNE J.D., AMANATIDES P.G., BRANDON R.C., ROGERS Y.,
EVANS C.A., GOALBYNE J.D., BALDWIN D., BANZON J., BEESON K.Y., BUSAM D.A.,
BANZON J., AN H., BALDWIN D., BANZON J., BEESON K.Y., BUSAM D.A.,
CARLSON J.W., CENTER A., CHAMPE M., DAVENPORT L.B., DIETZ S.M.,
DODSON K., DORSETT V., DOUP L.E., DOYLE C., DRENEK D., FARFAN D.,
FERRIERA S., FRISSE E., GALLE R.F., GAIG N.S., GEORGE R.A.,
GONZALEZ M., HOUCK J., HOSKINS R.A., HOSTIN D., HOWLAND T.J.,
IBEGWAM C., JALALI M., KRUSE D., LI P., MATTEI B., MOSHREFI A.,
IBEGWAM C., JALALI M., KRUSE D., LI P., MATTEI B., MOSHREFI A.,
MCINTOSH T.C., MOY M., MURPHY B., NELSON C., NELSON K.A., NUNCO J.,
PACLEB J., PARAGAS V., PARK S., PATEL S., PEIFFER B.,
PHOUANAVONG S., PITTMAN G.S., PURI V., RICHARDS S., SCHEELER F.,
STAPLETON M., STRONG R., SVIRSKAS R., TECTOR C., TYLER D.,
WILLIAMS S.M., ZAVERI J.S., SMITH H.O., VENTER J.C., RUBIN G.M.;
"Sequencing of *Drosophila melanogaster* genome";
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RP MISRA S., CROSBY M.A., MATTHEWS B.B., BAYRAKTAROGU L., CAMPBELL K.,
RA HRADCKY P., HUANG Y., KAMINKER J.S., PROCHNIK S.E., SMITH C.D.,
RA TUPY J.L., BERGMAN C., BERMAN B., CARLSON J.W., CELNIKER S.E.,
RA CLAMP M., DRYSDALE R., EMERT D., FRISE E., DE GREY A., HARRIS N.,
RA KROMMILLER B., MARSHALL B., MILLBURN G., RICHTER J., RUSSO S.,
RA SEARLE S.M.J., SMITH E., SHU S., SMUTNIAK F., WHITFIELD E.,
RA ASHBURNER M., GALBART W.M., RUBIN G.M., MUNGALL C.J., LEWIS S.E.;
"Annotation of *Drosophila melanogaster* genome";
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE FROM N.A.
RP ADAMS M.D., CELNIKER S.E., GIBBS R.A., RUBIN G.M., VENTER C.J.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A.
RP FlyBase;
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003488; AAF48147.2; -;
DR FlyBase; FBGN0030376; CG2750.
DR InterPro; IPR004325; Nucleoporin FG.
DR Pfam; PF03093; Nucleoporin FG; 10.
SQ SEQUENCE 1860 AA; 206779 MW; 049353971B7141272 CRC64;

Query Match 5.4%; Score 8; DB 5; Length 1860;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ISISKOLA 45
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Db 1692 ISISKOLA 1699

RESULT 11

20 AIATTALI 27

RESULT 9

Q49525 PRELIMINARY; PRF; 1365 AA.

Q49525; 01-NOV-1996 (TrEMBLrel. 01, Created)

Q49525; 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

Q49525; 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

Lmp1.

Lmp1.

Mycoplasma hominis.

Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

NCBI_TaxID=2098;

[1]

SEQUENCE FROM N.A.

STRAIN=M56;

MEDLINE=95369882; PubMed=7543881;

Jensen L.T., Ladefoged S., Birkelund S., Christiansen G.,
"Selection of Mycoplasma hominis PG1 deletion mutants by cultivation
in the presence of monoclonal antibody 552.";
EMBL; U21962; AAA81013.1; -;
PIR; T30822; T30822.

InterPro; IPR005864; LMP.

Pfam; PF04778; LMP; 4.

SEQUENCE 1365 AA; 154983 MW; 847A04992410867F CRC64;

Query Match 5.4%; Score 8; DB 2; Length 1365;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 AIATTALI 66
|||||

Db 20 AIATTALI 27

RESULT 10

Q9VVP5 PRELIMINARY; PRF; 1860 AA.

Q9VVP5; 01-MAY-2000 (TrEMBLrel. 13, Created)

Q9VVP5; 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

Q9VVP5; 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

CG2750 protein.

CG2750.

Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephidroides; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

[1]

SEQUENCE FROM N.A.

RP STRAIN=Berkeley;

RC MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Cocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Held G., Nelson C.R., Miklos G.L.G.,
RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrieli A.E., Gaig N.S., Galbart W.M., Glasser K.,
RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harteis J., Heiman T.J., Hernandez J.R., Houck J., Holt R.A.,
RA Holtin D., Houston K.A., Howland T.J., Wei M.-H., Ibgwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.J., Pacle J.M.,
RA Palazzo R.M., Pittman G.S., Pan S., Pollard D.R., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of *Drosophila melanogaster*";
SEQUENCE 287:2195-2195(2000).
[2]
SEQUENCE FROM N.A.
RP CELINIKER S.E., ADAMS M.D., KRONMILLER B., WAN K.H., HOLT R.A.,
CELINIKER S.E., COCAYNE J.D., AMANATIDES P.G., BRANDON R.C., ROGERS Y.,
EVANS C.A., GOALBYNE J.D., BALDWIN D., BANZON J., BEESON K.Y., BUSAM D.A.,
BANZON J., AN H., BALDWIN D., BANZON J., BEESON K.Y., BUSAM D.A.,
CARLSON J.W., CENTER A., CHAMPE M., DAVENPORT L.B., DIETZ S.M.,
DODSON K., DORSETT V., DOUP L.E., DOYLE C., DRENEK D., FARFAN D.,
FERRIERA S., FRISSE E., GALLE R.F., GAIG N.S., GEORGE R.A.,
GONZALEZ M., HOUCK J., HOSKINS R.A., HOSTIN D., HOWLAND T.J.,
IBEGWAM C., JALALI M., KRUSE D., LI P., MATTEI B., MOSHREFI A.,
IBEGWAM C., JALALI M., KRUSE D., LI P., MATTEI B., MOSHREFI A.,
MCINTOSH T.C., MOY M., MURPHY B., NELSON C., NELSON K.A., NUNCO J.,
PACLEB J., PARAGAS V., PARK S., PATEL S., PEIFFER B.,
PHOUANAVONG S., PITTMAN G.S., PURI V., RICHARDS S., SCHEELER F.,
STAPLETON M., STRONG R., SVIRSKAS R., TECTOR C., TYLER D.,
WILLIAMS S.M., ZAVERI J.S., SMITH H.O., VENTER J.C., RUBIN G

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 106 ILSELDE 112
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|
|
Db 103 ILSELDE 109

RESULT 13

QY Q7URHO PRELIMINARY; PRT; 114 AA.

ID Q7URHO

AC Q7URH0;
01-OCT-2003 (TREMELrel. 25, Created)

DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Probable molybdopterin-synthase sulfurylase.

GN MOEB OR R85670.

OS Rhodopirellula baltica.

OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;

OC Planctomycetaceae; Pirellula.

OX NCBI_TaxID=117;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=1;

RX MEDLINE=22735913; PubMed=12835416;

RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,

RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,

RA Schlesner H., Amann R., Reinhardt R.;

RT "Complete genome sequence of the marine planctomycete Pirellula sp.

RT strain 1."

RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).

DR EMBL; EX294142; CAD74368.1; -.

KW Complete proteome.

SQ SEQUENCE 114 AA; 12973 MW; 4627CA7401LC344D CRC64;

Query Match 4.8%; Score 7; DB 16; Length 114;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 LSELDEH 113
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|
|
|
Db 57 LSELDEH 63

RESULT 14

QY Q94ZD6 PRELIMINARY; PRT; 116 AA.

ID Q94ZD6

AC Q94ZD6;
01-DEC-2001 (TREMELrel. 19, Created)

DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE NADH dehydrogenase subunit 3.

GN NADH3.

OS Eptatretus burgeri (Inshore hagfish).

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;

OC Myxinidae; Eptatretinae; Eptatretus.

OX NCBI_TaxID=7764;

RN [1]

RP SEQUENCE FROM N.A.

RA Delarbre C., Gallut C., Barriel V., Janvier P., Gachelin G.;

RT "Phylogenetic resolution of cyclostomes using the mitochondrial DNA

RT sequence of the hagfish Eptatretus burgeri."

RL Submitted (JUN-2000) to the EMBL/GenBank/DBS databases.

DR ENBL; AJ278504; CAC42109.1; -.

DR GO; GO:0005739; C:mitochondrion; IEA.

DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.

DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u...; IEA.

DR InterPro; IPR000440; Oxidored_q4.

DR Pfam; PF00507; oxidored_q4; 1.

KW Mitochondrion.

SQ SEQUENCE 116 AA; 13277 MW; BFF4FIAD9297233B CRC64;

Query Match 4.8%; Score 7; DB 8; Length 116;
Best Local Similarity 100.0%; Pred. No. 52;

Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 ILLLSIT 131
Db 5 ILLLSIT 11

RESULT 15

Q7V175
ID Q7V175 PRELIMINARY; PRT; 130 AA.
AC Q7V175;
DT 01-OCT-2003 (TREMELrel. 25, Created)
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Hypothetical precursor.
GN PM1008.
OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococaceae;
OC Prochlorococcus.
OX NCBI_TaxID=59919;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642;
RA Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
niche differentiation."
RL Nature 424:1042-1047(2003).
DR EMBL; BX572092; CAB19467.1; --
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1..23
SQ SEQUENCE 130 AA; 14889 MW; 0D8681ADCAF81E77 CRC64;

Query Match 4.8%; Score 7; DB 16; Length 130;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 MILLLSI 130
Db 1 MILLLSI 7

Search completed: June 3, 2004, 13:30:21
Job time : 41 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2004, 13:23:07 ; Search time 18 Seconds
(without alignments)
425.240 Million cell updates/sec

Title: US-09-744-197-1

Perfect score: 147

Sequence: 1 MGGCMHSTQDKSLHLEGP.....LSITVMSDLLQNIERNVKIMK 147

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	8	5.4	433	1 HXB3_MOUSE	P09026 mus musculus
2	7	4.8	161	1 LEPA_PSEFL	P26843 pseudomonas
3	7	4.8	182	1 AREF_YEAST	P40994 saccharomyc
4	7	4.8	322	1 RL40_LUPLU	P50345 lupinus lut
5	7	4.8	346	1 PER9_ARATH	Q96512 arabidopsis
6	7	4.8	370	1 LEU3_RHIME	Q92ky8 rhizobium m
7	7	4.8	370	1 PRIL_AECFU	Q29911 archaeglob
8	7	4.8	429	1 YHG3_YEAST	P38756 saccharomyc
9	7	4.8	431	1 HXB3_HUMAN	P14651 homo sapien
10	7	4.8	439	1 PROA_SYNEL	Q8dku1 synechococc
11	7	4.8	469	1 GATE_TRETH	Q9lxc2 thermus the
12	7	4.8	497	1 C71G_ARATH	Q9fh66 arabidopsis
13	7	4.8	504	1 SH2E_MOUSE	Q02152 mus musculus
14	7	4.8	519	1 SYH_FUGRU	P70076 fugu rubrip
15	7	4.8	573	1 DPA1_SYNY3	Q55393 synechocyst
16	7	4.8	614	1 LEPA_CXBU	Q83bk3 coxiella bu
17	7	4.8	618	1 CHEA_LISIN	Q92dw2 listeria in
18	7	4.8	618	1 CHEA_LISMO	Q48768 listeria mo
19	7	4.8	813	1 ARM_MUSDO	Q02453 musca domes
20	7	4.8	980	1 UBE4_CAREL	Q09349 xenopus habi
21	7	4.8	1807	1 UTA2_XENLA	P18709 xenopus lae
22	7	4.8	3023	1 POLG_TVMV	P09814 t genome po
23	6	4.1	44	1 PSBN_CHLVU	P56326 chlorella v
24	6	4.1	64	1 RL37_LVCES	P49212 lycopersico
25	6	4.1	65	1 ICE2_ASCSU	P07852 ascaris suu
26	6	4.1	65	1 PAPE_PHYAM	P81418 phytolacca
27	6	4.1	69	1 COXR_PAPHA	Q8sq78 papio hamad
28	6	4.1	72	1 RL15_BACLI	P35138 bacillus li
29	6	4.1	78	1 Y270_METJA	Q57718 methanococc
30	6	4.1	92	1 FNR_CAPOC	Q46158 capnocytoph
31	6	4.1	92	1 FNR_CAPSP	Q46159 capnocytoph
32	6	4.1	92	1 FNR_HAASP	Q47948 haemophilus
33	6	4.1	93	1 S10A_MOUSE	P56565 mus musculus

34	6	4.1	93	1 S10A_RAT	P35467 rattus norv
35	6	4.1	97	1 HFO_NEIMA	Q9jgw6 neisseria m
36	6	4.1	100	1 YNO5_YEAST	P53906 saccharomyc
37	6	4.1	102	1 YE07_METH	Q27458 methanobact
38	6	4.1	110	1 LZ8_GALNU	P14945 ganoderma l
39	6	4.1	112	1 UCN2_HUMAN	Q96tp3 homo sapien
40	6	4.1	120	1 RL18_TREPA	O83335 treponema p
41	6	4.1	128	1 COTV_BACSU	Q08309 bacillus su
42	6	4.1	129	1 MINK_HUMAN	P15382 homo sapien
43	6	4.1	134	1 ATPE_DBSVM	Q985b5 desulfovibr
44	6	4.1	136	1 L5E2_HUMAN	O43716 homo sapien
45	6	4.1	138	1 Y560_METJA	Q57980 methanococc

ALIGNMENTS

RESULT 1

HXB3_MOUSE STANDARD; PRT; 433 AA.

AC P09026; P10285; Q61680;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B3 (Hox-2.7) (MH-23).
GN HOXB3 OR HOXB-3 OR HOX-2.7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92258392; PubMed=1582411;
RA Sham W.H.; Hunt P.; Nonchev S.; Papalopulu N.; Graham A.;
RA Boncinelli E.; Krumlauf R.;
RT "Analysis of the murine Hox-2.7 gene: conserved alternative
transcripts with differential distributions in the nervous system and
the potential for shared regulatory regions.";
RL EMBL J. 11:1825-1836(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95196953; PubMed=7890121;
RA Brown W.M.; Taylor G.R.;
RT "The 5'-sequence of the murine Hox-b3 (Hox-2.7) gene and its intron
contain multiple transcription-regulatory elements.";
RL Int. J. Biochem. 26:1403-1409(1994).
RN [3]
RP SEQUENCE OF 152-361 FROM N.A.
RX MEDLINE=88054465; PubMed=2890503;
RA Lonai P.; Arman E.; Czosnek H.; Ruddle F.H.; Blatt C.;
RT "New murine homeoboxes: structure, chromosomal assignment, and
differential expression in adult erythropoiesis.";
RL DNA 6:409-418(1987).
RN [4]
RP SEQUENCE OF 181-265 FROM N.A.
RX MEDLINE=89091992; PubMed=2463210;
RA Graham A.; Papalopulu N.; Lorimer J.; McVey J.H.; Tuddenham E.G.D.;
RA Krumlauf R.;
RT "Characterization of a murine homeo box gene, Hox-2.6, related to the
Drosophila Deformed gene.";
RL Genes Dev. 2:1424-1438(1988).
CC -!- FUNCTION: Sequence-specific transcription factor which is part of
a developmental regulatory system that provides cells with
specific positional identities on the anterior-posterior axis.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the Antp homeobox family.
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CC -----
DR ENBL; X66177; CAA46951.1; -
DR ENBL; U02276; AAB60496.1; -
DR ENBL; M8168; AAA37840.1; -
DR PIR; S20963; S20963.
DR HSP; P02833; ISAN.
DR TRANSFAC; T01724; -
DR MGD; MGI:96184; Hoxb3.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR PRINTS; PR00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT SITE 129 134 ANTP-TYPE HEXAPEPTIDE.
FT DOMAIN 154 181 GLY-RICH.
FT DNA BIND 191 250 HOMEBOX.
FT CONFLICT 113 113 G -> C (IN REF. 1).
FT CONFLICT 119 119 A -> S (IN REF. 1).
FT CONFLICT 152 168 GCGGGGGGGGGGGGG -> RLWWRPAVVAANAAR
(IN REF. 3).
FT CONFLICT 182 182 D -> N (IN REF. 4).
FT CONFLICT 216 217 LC -> FV (IN REF. 3).
FT CONFLICT 330 330 S -> L (IN REF. 3).
FT CONFLICT 342 361 GAYGTPMOGSPVVGGGY -> APTGPPCAVRCMAG
VAT (IN REF. 3).
SQ SEQUENCE 433 AA; 44353 MW; 9AD3C922663612A6 CRC64;

Query Match 5.4%; Score 8; DB 1; Length 433;
Best Local Similarity 100.0%; Pred.No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 PSAAPTST 28
| | | | |
DB 92 PSAAPTST 99

RESULT 2
LEPA_PSEFL STANDARD; PRT; 161 AA.
AC P26843;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE GTP-binding protein lepa (Fragment).
GN LEPA.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 10586;
RA Black M.T., Munn J.G.R., Allsop A.E.;
RT "On the catalytic mechanism of prokaryotic leader peptidase 1.";
RL Biochem. J. 282:539-544(1992).
CC -!- SUBCELLULAR LOCATION: PRESENT IN THE CYTOPLASM AND IS
CC ALSO FOUND IN THE PERIPLASM (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC Lepa subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X56466; CAA39838.1; -
DR PIR; S36880; S36880.
DR HAMAP; MF_000711; -; 1.
DR InterPro; IPR000795; EF_GTPbind.
DR InterPro; IPR000640; EFG_C.
DR InterPro; IPR009022; EFG_III_V.
DR Pfam; PF00679; EFG_C; 1.
DR PROSITE; PS00301; EFATOR_GTP; PARTIAL.
KW Membrane; GTP-binding.
FT NON_TER 1
SQ SEQUENCE 161 AA; 18210 MW; 5FB6924B6C47BB50 CRC64;

Query Match 4.8%; Score 7; DB 1; Length 161;
Best Local Similarity 100.0%; Pred.No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 SVKALRK 52
| | | | |
DB 106 SVKALRK 112

RESULT 3
ARF3_YEAST STANDARD; PRT; 182 AA.
ID ARF3_YEAST
AC P40994;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE ADP-ribosylation factor 3.
GN ARF3 OR YOR094W OR YOR3172W
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94342251; PubMed=8063710;
RA Lee F.-J.S., Stevens L.A., Kao Y.L., Moss J., Vaughan M.;
RT "Characterization of a glucose-repressible ADP-ribosylation factor 3
RT (ARF3) from Saccharomyces cerevisiae.";
RL J. Biol. Chem. 269:20931-20937(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97344368; PubMed=9200815;
RA Voss H., Benes V., Andrade M.A., Valencia A., Rechmann S., Teodoru C.,
RA Schwager C., Paces V., Sander C., Ansorge W.;
RT "DNA sequencing and analysis of 130 kb from yeast chromosome XV.";
RL Yeast 13:655-672(1997).
CC -!- FUNCTION: GTP-binding protein that functions as an allosteric
CC activator of the cholela toxin catalytic subunit, an ADP-
CC ribosyltransferase. Involved in protein trafficking; may modulate
CC vesicle budding and uncoating within the Golgi apparatus.
CC -!- SIMILARITY: Belongs to the small GTPase superfamily. Arf family.
CC -----
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CC -----
DR EMBL; J28996; AAA61614.1; -
DR EMBL; X94335; CAA64016.1; -
DR EMBL; Z75002; CAA99291.1; -
DR PIR; A53917; A53917.
DR HSP; P32889; IRRP.
DR GerMOnline; 143682; -
DR SGD; S0005620; ARF3.
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DR InterPro; IPR006688; ARF.
 DR InterPro; IPR006689; ARF/SAR.
 DR InterPro; IPR001806; Ras trnsfrmg.
 DR InterPro; IPR005225; Small_GTP.
 DR Pfam; PF00025; arf; 1.
 DR PRINTS; PRO00449; RASTRNSFRMG.
 DR PRINTS; PRO0328; SARIGTPBP.
 DR SMART; SM00177; ARF; 1.
 DR TIGRFAMs; TIGR00231; small_GTP; 1.
 DR PROSITE; PS01019; ARF; 1.
 KW GTP-binding; Multigene family; Myristate; Protein transport;
 FT INTR_MET 0 0
 FT LIPID 1 1 N-myristoyl glycine (Potential).
 FT NP_BIND 23 30 GTP (BY SIMILARITY).
 FT NP_BIND 66 70 GTP (BY SIMILARITY).
 FT NP_BIND 125 128 GTP (BY SIMILARITY).
 SQ SEQUENCE 182 AA; 20565 MW; 6B8370128369A270 CRC64;
 Query Match 4.8%; Score 7; DB 1; Length 182;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 61 ATTALIF 67
 DB 83 ATTALIF 89
 RESULT 4
 ID RLAO LUPLU STANDARD; PRT; 322 AA.
 AC P0345;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 60S acidic ribosomal protein P0.
 OS Lupinus luteus (Yellow lupine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids I; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
 OX NCBI_TaxID=3873;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Ventus;
 RX MEDLINE=98163879; PubMed=9503149;
 RA Mikolajczyk K., Barciszewski J.;
 RT "Expression of the cDNA and purification of P0 ribosomal protein from
 Lupinus luteus.";
 RL Biochem. Mol. Biol. Int. 44:69-77(1998).
 CC -!- FUNCTION: Ribosomal protein P0 is the functional equivalent of
 E.coli protein L10.
 CC -!- SUBUNIT: P0 forms a pentameric complex by interaction with dimers
 of P1 and P2 (By similarity).
 CC -!- SIMILARITY: Belongs to the L10P family of ribosomal proteins.
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 CC
 DR EMBL; X93587; CAA63786.1; -
 DR InterPro; IPR001813; Ribosomal_60S.
 DR InterPro; IPR001790; Ribosomal_L10.
 DR Pfam; PF00428; 60S ribosomal; 1.
 DR Pfam; PF00466; Ribosomal_L10; 1.
 KW Ribosomal protein; Phosphorylation.
 SQ SEQUENCE 322 AA; 34453 MW; DA8566209B5FC0BC CRC64;
 Query Match 4.8%; Score 7; DB 1; Length 322;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 PNPSAAP 25
 DB 235 PNPSAAP 241
 RESULT 5
 ID PER9 ARATH STANDARD; PRT; 346 AA.
 AC Q96512; Q9LPD4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Peroxidase 9 precursor (EC 1.11.1.7) (Atperox P9) (ATPI8a).
 GN PER9 OR P9 OR At1G44970 OR F27F5.6 OR T22C22.24.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Welinder K.G., Jespersen H.M., Kjaersgaard I.V.H., Justesen A.F.,
 OA Oestergaard L., Abelskov A.K., Hansen L.N., Rasmussen S.K.;
 RT "Prom expressed sequence tags to structure, function, evolution and
 expression of 29 ER-targeted Arabidopsis peroxidases.";
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Pederspiel N.A., Kaul S.,
 RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Dewar K.,
 RA Chung M.K., Conn L., Conway A.B., Feng J.-D., Fong B., Fujii C.Y.,
 RA Dunn P., Egtu P., Feldblum T.V., Feng J.-D., Hansen N.F., Hughes B., Huizar L.,
 RA Giller J.E., Goldsmith A.D., Haas B., Hansen N.F., Shinn P., Southwick A.M.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
 RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana.";
 RL Nature 408:816-820(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Brever V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.A.;
 RT "Full-length cDNA from Arabidopsis thaliana.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP CHARACTERIZATION.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=98409321; PubMed=9738941;
 RA Oestergaard L., Pedersen A.G., Jespersen H.M., Brunak S.,
 RA Welinder K.G.;
 RT "Computational analyses and annotations of the Arabidopsis peroxidase
 gene family.";
 RL FEBS Lett. 433:98-102(1998).
 RN [5]
 RP GENE FAMILY ORGANIZATION, AND NOMENCLATURE.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=22030461; PubMed=12034502;
 RA Tognolli M., Penel C., Greppin H., Simon P.;
 RT "Analysis and expression of the class III peroxidase large gene family

RT in Arabidopsis thaliana. ";
RL Gene 288:129-138(2002).
CC -!- FUNCTION: Removal of H(2)O(2), oxidation of toxic reductants,
CC biosynthesis and degradation of lignin, suberization, auxin
CC catabolism, response to environmental stresses such as wounding,
CC pathogen attack and oxidative stress. These functions might be
CC dependent on each isozyme/isoform in each plant tissue.
CC -!- CATALYTIC ACTIVITY: Donor + H(2)O(2) = oxidized donor + 2 H(2)O.
CC -!- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group and 2
CC calcium ions per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- MISCELLANEOUS: There are 73 peroxidase genes in A.thaliana.
CC -!- SIMILARITY: Belongs to the peroxidase family. Classical plant
CC (class III) peroxidase subfamily.
CC
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CC
CC EMBL; X59804; CAA67336.1; -;
CC EMBL; AC007915; AAF69153.1; -;
CC EMBL; AC020576; AAF78280.1; -;
CC EMBL; AY086626; AAM63684.1; -;
CC HSP; P22195; 1SCH.
CC InterPro; IPR002016; Peroxidase.
CC Pfam; PF00141; peroxidase; 1.
CC PRINTS; PR00459; PEROXIDASE.
CC PROSITE; PS00435; PEROXIDASE 1; 1.
CC PROSITE; PS00436; PEROXIDASE 2; 1.
CC PROSITE; PS50873; PEROXIDASE 4; 1.
CC Oxidoreductase; Glycoprotein; Peroxidase; Iron; Heme;
CC Multigene family; Calcium; Signal.
CC SIGNAL 1 23 POTENTIAL.
CC CHAIN 24 346 PEROXIDASE 9.
CC METAL 86 86 CALCIUM 1 (BY SIMILARITY).
CC METAL 89 89 CALCIUM 1 (VIA CARBONYL OXYGEN)
CC METAL 91 91 CALCIUM 1 (VIA CARBONYL OXYGEN)
CC METAL 91 91 CALCIUM 1 (BY SIMILARITY).
CC METAL 93 93 CALCIUM 1 (BY SIMILARITY).
CC METAL 95 95 CALCIUM 1 (BY SIMILARITY).
CC METAL 213 213 CALCIUM 2 (BY SIMILARITY).
CC METAL 264 264 CALCIUM 2 (BY SIMILARITY).
CC METAL 267 267 CALCIUM 2 (BY SIMILARITY).
CC METAL 272 272 CALCIUM 2 (BY SIMILARITY).
CC ACT SITE 81 81 BY SIMILARITY.
CC ACT SITE 85 85 DISTAL HISTIDINE.
CC ACT SITE 113 113 HYDROGEN-BOUND (BY SIMILARITY).
CC ACT SITE 182 182 SUBSTRATE BINDING (BY SIMILARITY).
CC METAL 212 212 IRON (HEME AXIAL LIGAND).
CC ACT SITE 289 289 HYDROGEN-BOUND (BY SIMILARITY).
CC DISULFID 54 134 BY SIMILARITY.
CC DISULFID 87 92 BY SIMILARITY.
CC DISULFID 140 342 BY SIMILARITY.
CC DISULFID 219 251 BY SIMILARITY.
CC CARBOHYD 185 185 N-LINKED (GLCNAC...) (POTENTIAL).
CC CONFLICT 269 269 A -> S (IN REF. 3).
CC CONFLICT 290 290 E -> Q (IN REF. 3).
CC CONFLICT 302 302 A -> S (IN REF. 3).
CC SEQUENCE 346 AA; 37741 MW; 47EPD6297469A065 CRC64;
Query Match 4.8%; Score 7; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 77 LEKAIK 83
DB 65 LEKAIK 71

RESULT 6
LEU3_RHIME STANDARD; PRT; 370 AA.
ID LEU3_RHIME
AC Q92KY8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 3-isopropylmalate dehydrogenase (EC 1.1.1.85) (Beta-IPM dehydrogenase)
DE (IMDH) (3-IPM-DH).
GN LEUB OR R03310 OR SMC04405.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN (1)
RP SEQUENCE FROM N.A.
RC SFPAIN=1021.
RX MEDLINE=2136507; PubMed=11481430;
RA Capela D., Baricoy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Bolstad P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kias E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puchler A., Purnelle B., Ransperger U.,
RA Renard C., Thebault P., Vandebol M., Weidner S., Galibert F.;
RA "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC -!- FUNCTION: Catalyzes the oxidation of 3-carboxy-2-hydroxy-4-
CC methylpentanoate (3-isopropylmalate) to 3-carboxy-4-methyl-2-
CC oxopentanoate. The product decarboxylates to 4-methyl-2-
CC oxopentanoate.
CC -!- CATALYTIC ACTIVITY: 3-carboxy-2-hydroxy-4-methylpentanoate +
CC NAD(+) = 3-carboxy-4-methyl-2-oxopentanoate + NADH.
CC -!- PATHWAY: Leucine biosynthesis; third step.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the isocitrate and isopropylmalate
CC dehydrogenases family. LeuB subfamily 1.
CC
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CC
CC EMBL; AL591793; CAC47889.1; -;
CC HAMAP; MF_01033; -; 1.
CC InterPro; IPR001804; Isodh.
CC InterPro; IPR004429; LeuB.
CC Pfam; PF00180; isodh; 1.
CC TIGRFAMs; TIGR00169; leuB; 1.
CC PROSITE; PS00470; IDH_IMDH; 1.
CC Oxidoreductase; Leucine biosynthesis; NAD; Complete proteome.
CC SEQUENCE 370 AA; 39586 MW; 49566B394486D7FD CRC64;
Query Match 4.8%; Score 7; DB 1; Length 370;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 55 DLEKAI 61
DB 326 DLEKAI 332
RESULT 7
PRIL_ARCFU STANDARD; PRT; 370 AA.
ID PRIL_ARCFU
AC O29911;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Probable DNA primase large subunit (EC 2.7.7.-).

GN PRIB OR AF0336.

OS Archaeoglobus fulgidus.

OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;

OC Archaeoglobaceae; Archaeoglobus.

OX NCBI_TaxID=2234;

RN [1].

SEQUENCE FROM N.A.

RP STRAIN=VC-16 / DSM 4304 / ATCC 49558;

RC MEDLINE=98049343; PubMed=938947;

RR Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

RA Ketchum K.A., Dodson R.J., Winn M., Hickey E.K., Peterson J.D.,

RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyriades N.C.,

RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

RA Cotton P.M., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,

RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Galand S.A.,

RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,

RA Venter J.C.;

RT "The complete genome sequence of the hyperthermophilic, sulphate-

RT reducing archaeon Archaeoglobus fulgidus";

RL Nature 390:364-370(1997).

CC -!- FUNCTION: DNA primase is the polymerase that synthesizes small RNA

CC primers for the Okazaki fragments on both template strands at

CC replication forks during chromosomal DNA synthesis (By

CC similarity).

CC -!- SUBUNIT: Heterodimer of a small subunit and a large subunit (By

CC similarity).

CC -!- SIMILARITY: Belongs to the eukaryotic-type primase large subunit

CC family.

CC -----

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CC -----

CC EMBL; AE001081; AAB90898.1; -.

DR DR PIR; H69291; H69291.

DR TIGR; AF0336; -.

DR HAMAP; MF 00701; -; 1.

DR InterPro; IPR007238; DNA_primase_lrg.

DR Pfam; PF04104; DNA_primase_lrg; 1.

DR Transferrase; DNA_replication; DNA-directed RNA polymerase; Primosome;

KW Complete proteome.

SW SEQUENCE 370 AA; 42844 MW; 4369F68516EB90E CRC64;

QY Query Match 4.8%; Score 7; DB 1; Length 370;

DB Best Local Similarity 100.0%; Pred. No. 23;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 REILSEL 110

DB 270 REILSEL 276

|||||

|||||

RESULT 8

YHG3_YEAST

ID YHG3_YEAST STANDARD; PRT; 429 AA.

AC F38756;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Hypothetical 48.9 kDa protein in RPL14B-GPAL intergenic region.

GN YHR003C.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;

```

RN  SEQUENCE FROM N.A.
RA  Kidd K.K., Busygina V., Demille M.M.C., Speed W.C., Ruggeri V.,
RA  Kidd J.R., Pakstis A.J.;
RT  "Overall linkage disequilibrium in 33 populations for highly
RT  informative multistep haplotypes spanning the HOXB gene cluster.";
RL  Am. J. Hum. Genet. 67:235-235(2000).
RN  [4]
RN  SEQUENCE OF 188-253 FROM N.A.
RC  TISSUE=Placenta;
RX  MEDLINE=89378558; PubMed=2570724;
RA  Glampao A., Acampora D., Zappavigna V., Pannese M.,
RA  D'Esposito M., Care A., Faiella A., Stornaiuolo A., Russo G.,
RA  Simeone A., Boncinelli E., Paschle C.;
RT  "Differential expression of human HOX-2 genes along the anterior-
RT  posterior axis in embryonic central nervous system.";
RL  Differentiation 40:191-197(1989).
RN  [5]
RN  SEQUENCE OF 188-253 FROM N.A.
RC  MEDLINE=90215256; PubMed=2576652;
RA  Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,
RA  Gaudino G., Stornaiuolo A., Cafiero M., Faiella A., Simeone A.;
RT  "Organization of human class I homeobox genes.";
RL  Genome 31:745-756(1989).
CC  -!- FUNCTION: Sequence-specific transcription factor which is part of
CC  a developmental regulatory system that provides cells with
CC  specific positional identities on the anterior-posterior axis.
CC  -!- SUBCELLULAR LOCATION: Nuclear.
CC  -!- DEVELOPMENTAL STAGE: Expressed in whole embryos and fetuses at 5-9
CC  weeks from conception.
CC  -!- SIMILARITY: Belongs to the Antp homeobox family.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X16667; CAA34657.1; -
DR  EMBL; U59298; AAD10852.1; -
DR  EMBL; AF287967; AAG31555.1; -
DR  EMBL; X16175; CAA34297.1; -
DR  PIR; S07543; WJHU2G.
DR  HSSP; P02833; ISAN.
DR  TRANSFAC; T01723; -
DR  Genew; HGNC:5114; HOXB3.
DR  MIM; 142966; -
DR  InterPro; IPR001827; Antennapedia.
DR  InterPro; IPR001356; Homeobox.
DR  Pfam; PF00046; homeobox; 1.
DR  PRINTS; PR00025; ANTENNAPEDIA.
DR  PRINTS; PR00024; HOMEBOX.
DR  ProDom; PD000010; Homeobox; 1.
DR  SMART; SM00389; HOX; 1.
DR  PROSITE; PS00027; HOMEBOX_1; 1.
DR  PROSITE; PS00032; ANTENNAPEDIA; 1.
DR  PROSITE; PS50071; HOMEBOX_2; 1.
KW  Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW  Transcription regulation.
FT  SITE 129 134
FT  DOMAIN 154 178
FT  GLY-RICH.
FT  DNA_BIND 188 247
FT  HOMEBOX.
FT  CONFLICT 199 200
SQ  SEQUENCE 431 AA; 44344 MW; 941706EDCC2975E5 CRC64;

Query Match 4.8%; Score 7; DB 1; Length 431;
Best Local Similarity 100.0%; Pred.No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 PSAAPTS 27
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Db 92 PSAAPTS 98

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RESULT 10
ID PROA SYNEL STANDARD; PRT; 439 AA.
AC Q8DKU1;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Gamma-glutamyl phosphate reductase (GPR) (EC 1.2.1.41) (Glutamate-5-
DE semialdehyde dehydrogenase) (Glutamyl-gamma-semialdehyde
DE dehydrogenase) (GSA dehydrogenase).
GN PROA OR TLR0764.
OS Synechococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32046;
RN [1]
RN SEQUENCE FROM N.A.
RC MEDLINE=22225144; PubMed=12240834;
RX Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
CC -!- FUNCTION: Catalyzes the NADPH dependent reduction of L-gamma-
CC glutamyl 5-phosphate into L-glutamate 5-semialdehyde and
CC phosphate. The product spontaneously undergoes cyclization to form
CC 1-pyrroline-5-carboxylate.
CC -!- CATALYTIC ACTIVITY: L-glutamate 5-semialdehyde + phosphate +
CC NADPH(+) = L-gamma-glutamyl 5-phosphate + NADPH.
CC -!- PATHWAY: Proline biosynthesis; second step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
CC -!- SIMILARITY: Belongs to the gamma-glutamyl phosphate reductase
CC family.
CC -----
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CC -----
DR EMBL; AF005371; BAC08315.1; -
DR HAMAP; MF_00412; -; 1.
DR InterPro; IPR002086; Aldehyde dehydr.
DR InterPro; IPR000965; Gglut_pp_reduct.
DR Pfam; PF00171; aldedh; 1.
DR TIGRfam; TIGR00407; proA; 1.
DR PROSITE; PS01223; PROA; 1.
KW Oxidoreductase; Proline biosynthesis; NADP; Complete proteome.
SQ SEQUENCE 439 AA; 46857 MW; 7036EBC5C62245EC CRC64;

Query Match 4.8%; Score 7; DB 1; Length 439;
Best Local Similarity 100.0%; Pred.No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 55 DLEKAIA 61
|||||
DB 244 DLEKAIA 250

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RESULT 11
ID GATB THETH STANDARD; PRT; 469 AA.
AC O9LCX2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

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DE Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B
DE (EC 6.3.5.-) (Asp/Glu-ADT subunit B).
GN GATB.
OC Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OC NCBI_TaxID=274;
OX NCBI_TaxID=274;
RN [1]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=20374936; PubMed=10913601;
RA Becker H.D., Min B., Jacobi C., Racznik G., Pelaschier J., Roy H.,
RA Klein S., Kern D., Soell D.;
RT "The heterotrimeric Thermus thermophilus Asp-tRNA(Asn)
RT amidotransferase can also generate Gln-tRNA(Gln).";
RL FEBS Lett. 476:140-144(2000).
CC -1- FUNCTION: allows the formation of correctly charged Asn-tRNA(Asn)
CC or Gln-tRNA(Gln) through the transamidation of misacylated Asp-
CC tRNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both
CC of asparaginyl-tRNA or glutamyl-tRNA synthetases. The reaction
CC takes place in the presence of glutamine and ATP through an
CC activated phospho-Asp-tRNA(Asn) or phospho-Glu-tRNA(Gln).
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamyl-tRNA(Gln) + L-glutamine = ADP
CC + phosphate + L-glutamyl-tRNA(Gln) + L-glutamate.
CC -1- CATALYTIC ACTIVITY: ATP + L-asparaginyl-tRNA(Asn) + L-glutamine = ADP
CC + phosphate + L-asparaginyl-tRNA(Asn) + L-glutamate.
CC -1- SUBUNIT: Heterotrimer of A, B and C subunits (By similarity).
CC -1- SIMILARITY: Belongs to the gatB/gatE family. GatB subfamily.
CC -----
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CC -----
DE EMBL; AF202448; AAF91177.1; -.
DR HAMAP; MF_00121; -.
DR InterPro; IPR004413; GatB.
DR InterPro; IPR006107; GatB_cent.
DR InterPro; IPR006075; GatB_N.
DR InterPro; IPR003789; GatB_Yqey.
DR Pfam; PF01162; GatB_1.
DR Pfam; PF02934; GatB_N; 1.
DR Pfam; PF02637; GatB_Yqey; 1.
DR TIGRFAMs; TIGR00133; gatB; 1.
DR PROSITE; PS01234; GATB; 1.
DR Protein biosynthesis; Ligase.
KW PROTEIN biosynthesis; Ligase.
SQ SEQUENCE 469 AA; 52236 MW; 10D01DF9C9B0625 CRC64;
Query Match 4.8%; Score 7; DB 1; Length 469;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 KSLHLEG 17
DB 125 KSLHLEG 131
RESULT 12
C71G ARATH STANDARD; PRT; 497 AA.
AC Q9PH66;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome P450 71A16 (EC 1.14.-.-).
DE CYP71A16 OR AT5G42590 OR K16E1.6.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
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OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=sv. Columbia;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:31-63(2000).
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
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CC -----
DE EMBL; AB022210; BAB09330.1; -.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450_1.
DR PRINTS; PS00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Transmembrane; Heme; Multigene family.
FT TRANSMEM 1 21 POTENTIAL.
FT METAL 439 439 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT DOMAIN 163 168 POLY-SER.
SQ SEQUENCE 497 AA; 55627 MW; 9F712BB0ECE1A166 CRC64;
Query Match 4.8%; Score 7; DB 1; Length 497;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 73 SDGKLEK 79
DB 233 SDGKLEK 239
RESULT 13
ID 5H2B MOUSE STANDARD; PRT; 504 AA.
AC Q02152;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 5-hydroxytryptamine 2B receptor (5-HT-2B) (serotonin receptor)
DE (5-HT-2F) (NP75 protein).
DE HTR2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93050195; PubMed=1426253;
RA Loric S., Launay J.-M., Colas J.-F., Maroteaux L.;
RT "New mouse 5-HT2-like receptor. Expression in brain, heart and
RT intestine.";
RL FEBS Lett. 312:203-207(1992).
CC -1- FUNCTION: This is one of the several different receptors for 5-
CC hydroxytryptamine (serotonin), a biogenic hormone that functions
CC as a neurotransmitter, a hormone, and a mitogen. This receptor
CC mediates its action by association with G proteins that activate a
CC phosphatidylinositol-calcium second messenger system.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Intestine and heart, but also in brain and
CC kidney.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC Strongest to the other 5HT-2 subtype receptors.
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CC -----
CC EMBL: Z15119; CAA78824.1; -
CC PIR: S27269; S27269.
CC MGD; MGI1109323; Rcr2b.
CC GO; GO:0007507; P:heart development; IMP.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHDOPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
CC PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Multigene family; Lipoprotein; Palmitate.
CC DOMAIN 1 55 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 56 78 1 (POTENTIAL).
CC DOMAIN 79 90 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 91 112 2 (POTENTIAL).
CC DOMAIN 113 128 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 129 150 3 (POTENTIAL).
CC DOMAIN 151 170 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 171 191 4 (POTENTIAL).
CC DOMAIN 192 215 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 216 238 5 (POTENTIAL).
CC DOMAIN 239 323 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 324 344 6 (POTENTIAL).
CC DOMAIN 345 359 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 360 382 7 (POTENTIAL).
CC DOMAIN 383 504 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC DISULFID 127 206 BY SIMILARITY.
CC LIPID 396 396 S-palmitoyl cysteine (Potential).
CC SEQUENCE 504 AA; 56545 MW; 045A483E281ECD30 CRC64;

Query Match 4.8%; Score 7; DB 1; Length 504;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 SVKALRK 52
DB 403 SVKALRK 409

RESULT 14
ID SYH_FUGRU STANDARD; PRT; 519 AA.
AC P70076;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
DE (HISRS).
GN HARS OR HISS.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=96323249; PubMed=8710896;
RA Brenner S., Corrochano L.M.;
RT "translocation events in the evolution of aminoacyl-tRNA
RT synthetases."
RL Proc. Natl. Acad. Sci. U.S.A. 93:8485-8489(1996).

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CC ----- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) = AMP +
CC diphosphate + L-histidyl-tRNA(His).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
CC -----
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CC -----
CC EMBL: Z54243; CAA91012.1; -
CC InterPro; IPR004154; HCTP_anticondon.
CC InterPro; IPR004516; Hiss.
CC InterPro; IPR002314; tRNA-synt_2b.
CC InterPro; IPR006195; tRNA_ligase_II.
CC InterPro; IPR00738; WHEP-TRS.
CC Pfam; PF03129; HCTP_anticondon; 1.
CC Pfam; PF00587; tRNA-synt_2b; 1.
CC Pfam; PF00458; WHEP-TRS; 1.
CC TIGRFAMs; TIGR00442; Hiss; 1.
CC PROSITE; PS50862; AA tRNA LIGASE II; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
CC SEQUENCE 519 AA; 57913 MW; A1CBF5752070759E CRC64;

Query Match 4.8%; Score 7; DB 1; Length 519;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 EILSELD 111
DB 202 EILSELD 208

RESULT 15
ID DPAL_SUNY3 STANDARD; PRT; 573 AA.
AC Q55393;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Diflavin flavoprotein A 1 (EC 1.-.-.-) (SSATF573) (NADH:oxygen
DE oxidoreductase).
GN DPAL OR SLL0550.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RX Kaneko T., Tanaka A., Sato S., Kotani H., Suzuki T., Miyajima N.,
RT Sugita M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome."
RL DNA Res. 2:153-166(1995).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=98321624; PubMed=9660187;
RX Wasserfallen A., Ragetti S., Jouanneau Y., Leisinger T.;
RT "A family of flavoproteins in the domains Archaea and Bacteria."
RL Eur. J. Biochem. 254:325-332(1998).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=22050187; PubMed=12054744;
RX Vicente J.B., Gomes C.M., Wasserfallen A., Teixeira M.;
RT "Module fusion in an A-type flavoprotein from the cyanobacterium
RT Synechocystis condenses a multiple-component pathway in a single
RT polypeptide chain."
RL Biochem. Biophys. Res. Commun. 294:82-87(2002).
CC -!- FUNCTION: Mediates electron transfer from NADH to oxygen, reducing

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CC it to water. This modular protein has 3 redox cofactors, in other
CC organisms the same activity requires 2 or 3 proteins.
CC -|- COPACTOR: Binds 2 iron atoms and a variable amount of FAD and FMN
CC per monomer.
CC -|- SUBUNIT: Homodimer.
CC -|- MISCELLANEOUS: By homology with norV in E.coli, may be involved in
CC nitric oxide detoxification (By similarity).
CC -|- SIMILARITY: In the N-terminal section; belongs to the zinc
CC metallo-hydrolase family group 3.
CC -|- SIMILARITY: In the C-terminal section; belongs to the flavodoxin
CC reductase family.
CC -|- SIMILARITY: Contains 1 flavodoxin-like domain.
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CC -----
CC EMBL; D64003; BAA10483.1; -.
CC PIR; S75748; S75748.
CC InterPro; IPR001279; Blactamase-like.
CC InterPro; IPR008254; Flav_nitox_synth.
CC InterPro; IPR002583; Flav_nitox_synth.
CC InterPro; IPR001226; Flavodoxin.
CC InterPro; IPR009002; FMN binding.
CC Pfam; PF01613; Flav_nitox_synth.
CC Pfam; PF0753; lactamase B; 1.
CC PROSITE; PS50902; FLAVODOXIN LIKE; 1.
KW Transport; Electron transport; Oxidoreductase; Flavoprotein; FAD; FMN;
KW Metal-binding; Iron; Multigene family; Complete proteome.
FT DOMAIN 43 236 ZINC METALLO-HYDROLASE.
FT DOMAIN 265 401 FLAVODOXIN-LIKE.
FT DOMAIN 424 573 FLAVODOXIN-REDUCTASE-LIKE.
FT METAL 92 92 IRON 1 (BY SIMILARITY).
FT METAL 94 94 IRON 1 (BY SIMILARITY).
FT METAL 96 96 IRON 2 (BY SIMILARITY).
FT METAL 159 159 IRON 1 (BY SIMILARITY).
FT METAL 178 178 IRON 1 AND 2 (BY SIMILARITY).
FT METAL 236 236 IRON 2 (BY SIMILARITY).
SQ SEQUENCE 573 AA; 63506 MW; E31BE51028949E58 CRC64;

Query Match 4.8%; Score 7; DB 1; Length 573;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SDLEKAI 60
Db 416 SDLEKAI 424
|||||

Search completed: June 3, 2004, 13:29:30
Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2004, 13:30:28 ; Search time 43 Seconds
(without alignments)
961.786 Million cell updates/sec

Title: US-09-744-197-1
Perfect score: 147
Sequence: 1 MGGCMHSTQDKSLHLEGPEN.....LSITVMSDLLQNIIRNVKIMK 147

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1155919 seqs, 28133677 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Listing first 45 summaries

Database : Published Applications AA.*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	93.9	140	9	US-09-764-864-1447
2	138	5.4	314	9	US-09-978-274A-2
3	7	4.8	41	9	US-09-864-761-41438
4	7	4.8	123	12	US-10-424-599-199526
5	7	4.8	127	10	US-09-764-891-4168
6	7	4.8	162	15	US-10-094-749-2625
7	7	4.8	173	12	US-10-425-114-39200
8	7	4.8	180	12	US-10-425-114-55789
9	7	4.8	183	15	US-10-369-493-22366
10	7	4.8	188	14	US-10-106-698-5287
11	7	4.8	213	15	US-10-393-840-53
12	7	4.8	245	16	US-10-389-566-398
13	7	4.8	378	15	US-10-369-493-17232
14	7	4.8	414	12	US-10-425-114-52749
15	7	4.8	417	12	US-10-424-599-167317

16	7	4.8	496	12	US-10-425-114-51057	Sequence 51057, A
17	7	4.8	504	10	US-09-903-376-2	Sequence 2, Appli
18	7	4.8	552	12	US-10-425-114-58950	Sequence 58950, A
19	7	4.8	747	12	US-10-072-012-566	Sequence 566, App
20	7	4.8	790	15	US-10-369-493-21510	Sequence 21510, A
21	7	4.8	804	16	US-10-389-566-1940	Sequence 1940, App
22	7	4.8	890	15	US-10-369-493-23121	Sequence 23121, A
23	7	4.8	1311	8	US-08-954-701A-4	Sequence 4, Appli
24	7	4.8	1311	10	US-09-754-032-4	Sequence 4, Appli
25	7	4.8	1311	14	US-10-421-446-4	Sequence 4, Appli
26	7	4.8	19723	15	US-10-084-846A-5	Sequence 48, Appli
27	6	4.1	9	10	US-09-793-451-48	Sequence 263, App
28	6	4.1	9	10	US-09-793-451-263	Sequence 364, App
29	6	4.1	9	10	US-09-793-451-364	Sequence 415, App
30	6	4.1	9	10	US-09-793-451-415	Sequence 48, Appli
31	6	4.1	9	14	US-10-283-722-48	Sequence 263, App
32	6	4.1	9	14	US-10-283-722-364	Sequence 364, App
33	6	4.1	9	14	US-10-283-722-415	Sequence 415, App
34	6	4.1	9	15	US-10-283-903-48	Sequence 263, App
35	6	4.1	9	15	US-10-283-903-263	Sequence 364, App
36	6	4.1	9	15	US-10-283-903-364	Sequence 415, App
37	6	4.1	9	15	US-10-283-903-415	Sequence 50, Appli
38	6	4.1	9	15	US-10-428-335-50	Sequence 135, App
39	6	4.1	9	15	US-10-428-335-135	Sequence 398, App
40	6	4.1	10	10	US-09-793-451-398	Sequence 499, App
41	6	4.1	10	10	US-09-793-451-499	Sequence 503, App
42	6	4.1	10	10	US-09-793-451-503	Sequence 605, App
43	6	4.1	10	10	US-09-793-451-605	Sequence 693, App
44	6	4.1	10	10	US-09-793-451-693	
45	6	4.1	10	10	US-09-793-451-693	

ALIGNMENTS

RESULT 1
US-09-764-864-1447
; Sequence 1447, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1447
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-1447

Query Match 93.9%; Score 138; DB 9; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.9e-127;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 DKSLEHGDNPNSAAPTSTCAPKPKRISISKOLASVKALRKCSDLEKATATLIPRN 69
DB 3 DKSLEHGDNPNSAAPTSTCAPKPKRISISKOLASVKALRKCSDLEKATATLIPRN 62
QY 70 SSDSGKLEKAIADKLLQTFNFAEGQETPKYKREILSELDEHTENKLDFFEDFWILL 129
DB 63 SSDSGKLEKAIADKLLQTFNFAEGQETPKYKREILSELDEHTENKLDFFEDFWILL 122
QY 130 ITVMSDLLQNIIRNVKIMK 147
DB 123 ITVMSDLLQNIIRNVKIMK 140

RESULT 2
US-09-978-274A-2

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, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: US 60/234,687
, PRIOR FILING DATE: 2000-09-21
, PRIOR APPLICATION NUMBER: US 09/508,408
, PRIOR FILING DATE: 2000-06-30
, PRIOR APPLICATION NUMBER: US 09/774,203
, PRIOR FILING DATE: 2001-01-29
, NUMBER OF SEQ ID NOS: 49117
, SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
, SEQ ID NO 41438
, LENGTH: 41
, TYPE: PRT
, ORGANISM: Homo sapiens
, FEATURE:
, OTHER INFORMATION: MAP TO AC015525.3
, OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3
, OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.5
, OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
, OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
, OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.7
, OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6
, OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3
, OTHER INFORMATION: EST_HUMAN HIT: BE789681.1, EVALUATE 1.00e-07
, US-09-864-761-41438
Query Match 4.8%; Score 7; DB 9; Length 41;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0

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RESULT 4
US-10-424-599-199526
; Sequence 199526, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 199526
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(123)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_22197C.1.pep
US-10-424-599-199526

Query Match          4.8%; Score 7; DB 12; Length 123;
Best Local Similarity 100.0%; Pred.No. 87;
Matches              7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      49 ALRKCS D 55
Db      106 ALRKCS D 112
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RESULT 5
US-09-764-891-4168
; Sequence 4168, Application US/09764891

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Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4168
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-891-4168

Query Match 4.8%; Score 7; DB 10; Length 127;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 SAAPTST 28
Db 90 SAAPTST 96

RESULT 6
US-10-094-749-2625
; Sequence 2625, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYU
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2625
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2625

Query Match 4.8%; Score 7; DB 15; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 LASVKAL 50
Db 92 LASVKAL 98

RESULT 7
US-10-425-114-39200
; Sequence 39200, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 39200
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3079-017-B11_FLI.pep
US-10-425-114-39200

Query Match 4.8%; Score 7; DB 12; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 GKLEKAI 81
Db 76 GKLEKAI 82

RESULT 8
US-10-425-114-55789
; Sequence 55789, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 55789
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4698-005-G5_FLI.pep
US-10-425-114-55789

Query Match 4.8%; Score 7; DB 12; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 GKLEKAI 81
Db 79 GKLEKAI 85

RESULT 9
US-10-369-493-22366
; Sequence 22366, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22366
LENGTH: 183
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22366

Query Match 4.8%; Score 7; DB 15; Length 183;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 ATTALIF 67
Db 84 ATTALIF 90

RESULT 10
US-10-106-698-5287
Sequence 5287, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005PI
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 5287
LENGTH: 188
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: MISC FEATURE
LOCATION: (170)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC FEATURE
LOCATION: (172)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC FEATURE
LOCATION: (177)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC FEATURE
LOCATION: (183)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC FEATURE
LOCATION: (188)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-5287

Query Match 4.8%; Score 7; DB 14; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 ILSDELDE 112

Db 46 ILSDELDE 52

RESULT 11
US-10-393-840-53
Sequence 53, Application US/10393840
Publication No. US20030229922A1
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
TITLE OF INVENTION: Materials and Methods for the
FILE REFERENCE: 11000.1012c3
CURRENT APPLICATION NUMBER: US/10/393,840
CURRENT FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: US 09/636,800
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US 09/170,862
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 60/148,426
PRIOR FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT NZ/99/00169
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 956
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53
LENGTH: 213
TYPE: PRT
ORGANISM: Pinus radiata
US-10-393-840-53

Query Match 4.8%; Score 7; DB 15; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 GKLEKAI 81
Db 73 GKLEKAI 79

RESULT 12
US-10-389-566-398
Sequence 398, Application US/10389566
Publication No. US20040025202A1
GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 38-77(52900)D
CURRENT APPLICATION NUMBER: US/10/389,566
CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: PatentIn version 3.2
SEQ ID NO 398
LENGTH: 245
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc.feature
LOCATION: (21)..
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-389-566-398

Query Match 4.8%; Score 7; DB 16; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 GKLEKAI 81
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Db 91 GKLEKAI 97

RESULT 13

US-10-369-493-17232
; Sequence 17232, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17232
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-10-369-493-17232

Query Match 4.8%; Score 7; DB 15; Length 378;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 LEKAIAT 62
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Db 58 LEKAIAT 64

RESULT 14

US-10-425-114-52749
; Sequence 52749, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 52749
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700562414_FLI.pep
US-10-425-114-52749

Query Match 4.8%; Score 7; DB 12; Length 414;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 DGKLEKA 80
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Db 350 DGKLEKA 356

RESULT 15

US-10-424-599-167317
; Sequence 167317, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 167317
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_122104C.1.pep
US-10-424-599-167317

Query Match 4.8%; Score 7; DB 12; Length 417;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 DGKLEKA 80
|||||||
Db 353 DGKLEKA 359

Search completed: June 3, 2004, 13:36:14
Job time : 43 secs